

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
25984	56352	A	26125	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTSPILALPSYSTTTFGVC TSASMNVPVLTLRIRTRVTGEV AAIKPFSMANAPTFDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/VWAGTFD*SVWF GHDTDVVTLRYFHEALCYSVT LRTPHRRVLRFKSHQHPGELACFI SPVA
25985	56353	A	26126	905	4761	PPHNWMPSNATPGIAFVWCAY GAILPGDAPVPVDDYRKVVR KDTKGLIARWKYFWMVSIALG VAFALYLAGKDDPATQLVVPFF KDVMPQLGLFYILLA YFVIVGT GNAVNLTDGLDLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAVLLRQEFLLVIM GGVFVVETLSVLQVGSFKLRG QRIFRMAPIHHHYELKGWP
25986	56354	A	26127	1056	1373	
25987	56355	A	26128	1	301	SSGTAGRRYRPRQRPSPKSRNN RRVNRQPAQQSSRN/SLRPSTT SSPFSLPVAVKLPSAP/V* SAGMR LAEVRRVDSAISTVDSR* CPTAS SFSTGSITVTL
25988	56356	A	26129	362	595	
25989	56357	B	26130	1	1305	
25990	56358	A	26131	1	2022	MISKRSERSFGYGVGLVRRQDF SSSEGGFNLHSLRIDINKCLGVRI STATSTMGIVLPEQIKLACNGIQ RVALCGGDDYLTSDVSFDMVF CSRFGWQVRPSSFCSPVFTWVT ENQQLHRGKDNLSLKNNSA CGAACGSLRGEKSDPPSARNNP SSQGGKKESGQPSLKDPHIL RHDSAHRPRKEKPRQPVNASLV VKFVRVKCVCHNDHKRPACS VVCVDGDTYCWTEAYPAMGL PTLRGPDSALGERPE
25991	56359	A	26132	3	236	
25992	56360	B	26133	1	4638	
25993	56361	A	26134	1501	1914	SAFSRALTGROHFNNCAFTFRS NGAECLLYHVCQTAFVARRR VGAAGVGFSHIEIVPLHLLQQP LADLFVHVVARLSSTMGIRDQR PLPG*LLNNITRWRSSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
25994	56362	A	26135	561	698	

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25995	56363	B	26136	4	2040	
25996	56364	A	26137	804	947	LPCHCSCPWDGQVQSPSTRQ WT*GERLH*QSEALPGVCCAPG HGPL
25997	56365	A	26138	1	734	SVHIGHQFFQFQSTSLNICPPLH RLFIAPQMNIRRNAAARHAKFQ RLQAQVSIFEDDMSRKIANRQA TAMLNAPPEANIGIHNVPIGIF EAVIRQHFAARLNAFFALLFR PFRLFCPPGINANQRSQVRQPQ LPRLDITFQFWSWLSGGVDQRT VDIVCHQWRSALDRKEYYPAE TTMPTALHSRLCIIVGKIKRPVI VLFREANQARVGLFE/H*STAA RPFWSAAPAGPALPLRVANAPS
25998	56366	A	26139	2	309	
25999	56367	A	26140	472	885	SAFSRALTGRQHFNCAFRFS NGAECLLYHVQCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRSPVDTQ HSQSAGFAVTPENAFVASSGPS RHRHQR
26000	56368	A	26141	1	2469	
26001	56369	A	26142	1175	1435	
26002	56370	A	26143	218	443	AMARWKMLCTKSPPCVCLPGY P/G*RLAGPHHHHEFPPAGAAAS TGPPIVQDHQSLAGRSRRHDDS RHLGRCHHH
26003	56371	A	26144	1	2031	
26004	56372	A	26145	1419	1875	TFCSPRSQPSGLKRRRLRAGAGN CPLYSTGNGLQRAICCAQPT*L HGRVPSHVPAFTSSFQLWSFTV GACIHRSMYIISRSRCPDPKTK TATMLGITSFVMERCQLFILSRA FTSGQPTCYYPASSNTWFSST RHCQVINLHSNSMHISL
26005	56373	A	26146	218	441	AMARWKMLCTKSPPCVCLPGY P/G*RLAGPHHHHEFPPAGAAAS TGPPIVQDHQSLAGPRRHDDSR HLVRCHHH
26006	56374	A	26147	1196	1462	LNTLVVAVRDGLKMTTVIANN VTSVSVLKIARNVTRKTILPPAA AANVTYPWLIRTIC*KRRYD*K TRWYYA VAACLNCNMGTTRKA NG

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26007	56375	A	26148	45	443	APSPDKRDFPLPHGADSAMAE YDRCHRAVLSSQGGQWPTALSA GDHAAAYSLHAALVQPERRCHG RCPVRNRLHAPVCPPIPG*RPAG SHHHHEFPPPARAASTGPSIVQ DHQSLAGRSRRHDDPRHFGGC HHH
26008	56376	A	26149	581	957	TSWISFSRTTPSTVSPYSTVDAN GIIWSARNRLASVNNIASWLSFF SNFLYLAIKPNCLMMNRNGCS TPGPGCWLSCIRC*WAVCSCVD AASRFLPCRGARRSASPHPRQ APRRCGALW*PASAETNCSSPC SRLPS*LRGCCFKVLTLPGRSAI SQSTSTSASSALWRPLVAGIG
26009	56377	B	26150	1	3924	
26010	56378	A	26151	597	856	
26011	56379	B	26152	1	2781	
26012	56380	A	26153	2809	2989	RCGYVRE*LAKSLQSNHFQWR MPQHQTAYCRS*AWYRHVAH ERLPAQTDNRHQHADRWNQ
26013	56381	B	26154	1	2802	
26014	56382	A	26155	4493	5470	IQRRNHRRDGWCLASLPGTGD HAGARAEAGSWHSGGPHRVR ARSVSTPFAPIVNTATSLKPRV QLLDAALKIDHRRRTLKYSFGT FRRWYRSVAAQQAQYKDQVA FFHGCNVNYPQLGQDLIKVL NAMGTGVQLLSKEKCCGVPLI ANGFTDKARKQAITNVEISIREA VGVKIPVIATSSCTCFALRDEY PEVLNVNKGRLRDHIELANRW LWRKLEGGQTLPLKPMTLKVV YHTPCHME*MGWTLY/TLELLR NIPGLE/LTVLDSQ/CC/GIPPIRV VIHMFQIEESGADLVVTDCE CKWQIEMSTSLRCEHPITLLAQ ALA
26015	56383	A	26156	2467	3465	

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26016	56384	A	26157	5758	7019	LKEGLLEPLAVTERLAHRRWRP TMNDTSFENCICKTVCTTACPV SRVNPVPGPKQAGPDGERLRL KDGAlyDEALKYCINCKRCEV ACPSDVKIGDIIQRARAKYDIT RPSLRNFVLSHTDLMGSVSTPF APIVNTATSLKPVRLDALK IDHRRTLPKYSFGTFRRWYRSV AAQQAQYKQVAFHGFVNV YNHPQLGKDLIKVLNAMGTGV QLLSKEKCCGVPLIANGFTDK ARKQAITNVESIREAVGVKGIP VIATSTCTFALRDEYPEVLNV DNKGLRDHIELATRWLRKLD EGKTLPLKPLPLKVYYHTPCHM EKMGWTLTYTLELRNIPGLELT VLDSQCCGIAGTYGFKKENYPT SQAIGAPLFRQIEESGADLVTD CETCKWQIEMSTSLRCEHPITLL
26017	56385	B	26158	1	2247	
26018	56386	A	26159	882	2372	HAVHESPPCECRSNQQRPTRTCR TIIDIMEMYHALHVSWSNLQDQ QSIDERRVTLFGDAATEARYL GYVRFMVNVEGRYTHFDAGTH GFNAQTPMWEKYQRMNLNVWH ACPRFLFDLDGTLVDSLPAVER AWSNWARRHGLAPEEVLAFIH GKQAITSRLRHFMAGKSEADIAA EFTRLEHIEATETEGITALPGAIA LLSHLNKAASGVTKNGFLTVD EIRRVTRAFARLGTKEVRLTGG EPSLRDRDFTDIAAVRENDAIRQ IAVTTNGYRLERDVASWRDAG LTGINVSVDSLDRQFHAITGQ DKFNQVMAGIDAAFEAGFEKV KVNTVLMRDVNHHQLDTFLN WIQHRPIQLRFIELMETGEGSEL FRKHHISGQVLRDELLRRGWIH QLRQRSDDGPAQVFCHPDYAGEI GLIMPYDKDFCATCNRLRVSS IGKLHLCLFGEGGVNLRDLLED DTQQQALEARISAAALREKKQTH FLHQNNTGITQNLISYIGG
26019	56387	A	26160	68	399	NKVKPRGDSV/PGSPHSRLLSP PPLPGLLLWR/PLEEPFSPPLHC GSPFLGWPRPGGRGLGG/PPHSE QPASLSLPPTPRAPVRPEPPRA PPAPRRPVPSITQGLRNASAP

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26020	56388	A	26161	207	479	PWSDGAGPLPSLPHPDGRG*SV NSPQVLL**GSGE/PRASDSPLP QLCGVSPHRPTWGSALWGGEQ CTSEMGETIDPPGPHTFSKNFCF ELQ
26021	56389	B	26162	1	453	
26022	56390	A	26163	1	379	
26023	56391	A	26164	1	1054	MFLQAAQKAWNPHLLLVRTQ AASTHGRRADPHVGRGCTETPQ SWGKGESLALAPLSLTKAALED CSQISPSHQGTLLCLLILDRLTG KLSLEHTEEPSDVPSHLLYRWSI SSAITEVFQALASSDSTSQPVNV IITKEDMKVQDIALVLPKRKR NACRTTTSTCKALLMRQLAAR VILQNCVSKSSRGHVPQKNLT LPVRGDSVLAGSPHSRSLSAPP LPGLPLWRHLKSPSAHRCVTGG PFLGWPRPEPAPSACREALAAF P/PGQGS GPAAR/QPEPPPPWA PVQPESPRQAPPPAPRSPVSTT QGLRSTGTKHRDWQAAPPAAP VRDPLGEASWAPESGGDVENL
26024	56392	A	26165	2	362	EMSRLYRSRDRD/GVCLQ/IEVK MVSRTANIDDSLIGGNASAEA PEGEGTESTVTGVDIVMNHHL QETSFTKEAYKKYKDYMKSIK GKLEEQRPRDVKPFMTGAAEQI KHILANFKNYQ
26025	56393	A	26166	35	359	
26026	56394	A	26167	22	459	
26027	56395	B	26168	102	431	
26028	56396	A	26169	85	674	RRRLPSVAIMIILPGPSSSHDE MF/DSKIR/EAIDGVCAWKVE G/KMV/SRTE/GTID/DSLIGGNA SAERPRGAKGTERHQLITGV/DI VMTPHL/QETKFSQKEASKK/YI K/DYMKSIKRET*KNRRPEKSK TFL*PGA AEQ/KHILANFKNYQ FFIGENMNP/DGMVALLDYP*D WVVTYPMIFF*GWV*KWEKC
26029	56397	A	26170	1	1640	
26030	56398	A	26171	1	1527	

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26031	56399	A	26172	61	2560	PGFCHPRKAYSSYGQRSGSKQK MKASSGRGCLVRWLQVLLPFL LSLFPALPVQIRYSIPEELAKN SVVGNLAKDLGLSVRDLPAK LRVSAEKEYFTVNPESGDLVLS DRIDREQICGKQPLCVLDFDTV AENPLNIFYIAVIVQDINDNTPL FKQTKINLKIGESTKPGTTFPLD PALDSDVGPNSLQRYHLNDNE YFDLAEKQTPDGRKYPELILKH SLDREHSLHQLVLTAVDGGDP PQSGTTQIRIKVTDANDNPPVFS QDVYRVTLREDVPPGFFVLQVT ATDRDEGINAEITYSFHNVDEQ VKHFFNLNEKTGETTKDDLDF EIASSTYLSEAKDPGDAAHCS IQVEILDDNDCAPEVIVTSVSTP LPEDSPPGTVIALIKTRDRDSGE NGEVYCVLGNAKFILKSSSKN YYKLVTGDGALDREEIPEYNLTI TATDGGKPLSSIIIVTLHISDV NDNAPVFQQTSYMVHVAENNP PGASIAQISASDPDLGPGSQVSY SIVASDLKPREILSYVSVSAQSG VVFAQRAFDHEQLRAFELTLQ ARDQGSFALSANVSLRVLVGD LNDNAPRVLPALGPDGSALFD MVPRAAEPGYLVTKVVAVDA DSGHNAWLSYHVLQASEPGLF SLGLRTGEVRTARALGDRDAA RQRLLVAVRDGGQPPLSATATL HLIFADSLQEVLPDLSDRRREPSD
26032	56400	A	26179	47	325	ATMRLSVCLLLTLALCCYRA NAVVCQALGSEITGFLLAGKPV FKVQLAQFKAPVEAVASNMEA INCVDTMAYEKRVLITKTLGKI AEKCDR
26033	56401	A	26180	1	3747	
26034	56402	A	26181	2776	2874	
26035	56403	A	26182	89	369	
26036	56404	A	26183	382	555	
26037	56405	A	26184	2	67	
26038	56406	B	26185	1	444	
26039	56407	A	26186	1129	1275	
26040	56408	A	26187	61	313	WIPHQGYRWSCLPVPRCALAFL SPWVVDGTGHRGAGGGAGWG GFGRTGAHGIVGSGSGMAGCR SRAHSGGVGMTMTWQIPEVP

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26041	56409	A	26188	61	433	WIPHRGCRWWSCLPVPRGALAF SPRVVSGTGRRGAEGGARRGG SGRTGAHGVGGRLRHGGQLQVP SLAPREGSCTCGGSGSAREEQ NLGFPREPRSGGGARGSDGICG MRVMFRKWILFCPSRR
26042	56410	A	26189	297	599	
26043	56411	A	26190	370	585	
26044	56412	A	26191	222	799	
26045	56413	A	26192	346	634	
26046	56414	B	26193	206	955	
26047	56415	A	26194	281	549	
26048	56416	A	26195	1981	2337	
26049	56417	A	26196	267	770	TRVDMIHVGLRKGPGETPS*SL RSFRAGQGTGASRARGLTLLSSH SSALRKGSPPKHFTCLCWQTF LAWCVWVAFSPSRCTQTFDLGK STQWTLLEILTDPKSHLFSRKQ PQARAPAVFPAPLKGCHVGAR GSHCCQFGQCFRPSVAPLILGT DGFSLLEKLWTFKTC
26050	56418	A	26197	165	374	RVTVQWL*YLRPRMP*N*PRPR SGKPFIDSTHSSHR*RQRNAVSL FSPVMSALRRCSVHRRLPDGGV VA
26051	56419	A	26198	357	981	HWRGDVLRSHRRTALQSRYF CGIYRSP/YKAR/MQIQFFDPQQ MEAAQKRLTEESDILNALENHQ FAIWLPQVEMTSGLRGISKQ LVGFTNRQNGATKLLVQYFTH RQIDCAGTADQPNPAGKVDDC GVTGNVTDROQKQKHGQAKE NELQNAACAFQRAECHKQRKYA PQTQVDTKELCIWRIGQTQFRH QQNRNRQAERTNHFQVR
26052	56420	A	26199	1	2601	

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26053	56421	A	26200	1	1236	MGPGLDLPRLATFWTELGLLS WARELARMPAEMPPRSCPGR SRLSCSIGVAMFYGDLTAEQLY SRAISAAFTARHKGKNQIQFFD PQQMEAAQKRLTEESDILNALE NHQFAIWLPQVEMTSGKLP KSAAILPLSVNLSALQLMHPN MVADMLELLTRYRIQPTLILE VTESRRIDDPHAAVAIRPLRN AGVRVALDDFGMGYAGLRQL QHMKSLVRLTKSEVSSETDQDE LPLAKVSEVDEAKRQWLQGM HPVDVTVEPEPAEILAEFIRQHS AAGQLVARAVFLSPPYLVAEEE LSVLLESIKQNGDYADIACLTG SKDDYYYSTQAMSENAYAAMSL QVVEQDIFSPIAHAVRFECQTY PRPYKVAMLMQAPYYFQEAQI EAAIAAMDVAPEYADIRQGIVG
26054	56422	A	26201	1	1161	
26055	56423	A	26202	1	1038	
26056	56424	A	26203	1	1472	MVRLCIRLPVYAKVVDKNAL SLWMRERSDLWVQPKVDGVA VTLVYRDGKLNKAISRGNGLK GEDWTQKVSLSIAVPQTVSGLP ANSTLQGEIFLQREGHIQQQMG GINARAKVAGLMMRQDSDTL NSLGVFVWAWPDGPQLMSDRL KELATAGFTLTQTYTRAVKNA DEVARVRNEWWKAELPFVTD GVVVRAAKEPRIPPLATGPGRV AGGLEISTCSSGCRSEGNEPGKI SVVASLAPVMLDDKKVQVRNI GSVRRWQEWDIAPGDQILVSL AGQGIPRIDDVCPSPAILSDIVP SW/VTITQW/LKKRAVSSRMK NQ/VKKGSETGYFDKDEARFQK EGFRVVPAAALRQGAFIARNT LRPSYVNI GAYVDEGTMVDTW ATVGSACQIGKNVHLSAGVGIG GVLEPLQANPTIIEDNCFIGARS EVVEGVIVEEGSVISMGGVIGQ STRIYDRETGEIHYGRVP/AGKV DAKTRGKVGINELLRTID
26057	56425	A	26204	240	455	RLHPYPYRGWIFEVVPVISMGV YNGQSTRIYDR/ETGEIHYGRVP AGSVVVS/KVDAKTRGKVGINE LLRTID

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26058	56426	A	26205	197	1043	YEKSLTMQQLQNIETAFERRA EITPANADTVTREAVNQVIAL DSGALRVAEKIDGGVWVTHQWL KKAIVLLSFRINDNQVIEGAESR YFDKVPMPKFADYDEARFQKEG FRVVPAAVVRQGAFIARNTVL MPSYVNIQAYVDEGTMVDVW ATVGSQAQIGKNVILSGGVGI GGVLEPLQANPTIIEDNCFIGAR SEVVEGVIVEEGSVISMGVYIG QSTRIYDRETGEIHYGRVPAGS VVVSGNLPSKDGKYSLYCAVIV KKVDAKTRGKVGINELLRTID
26059	56427	A	26206	1	406	MGKKNWNTLGEVGCSCRMFL PDANTLAKNSACSAASAVQAA DRPDSQEAEELEHMAHSRCAL RCQTLVIVHSLMRVSWYHSLVI IVVPLTEPLESLVRCRLRSRRD DVPVAPAVSATPRREPISVLRIA ERTNA
26060	56428	A	26207	1	2574	MWAFRGKRPVTLKILHVPITNL RKNTSTRGLTKESSQGKLVRA QEEYTPAREIAKMG/GNPCRPG GIVFAGER*DVTSPPYV*TSRGL TKESSQGKLVRAQEEYTPAREI AKMGWQSLPARRYCLCWRKIR RYITLRLNIAYAGGYKAPVEDI ALWMETDGACDHVDFWTNIPS KCQGPMDIVSRPVFWAHGIV LFAGARNLNPTRLTRIPPYLWLL TLRTGYAAAGMQALALDSRGS PDVVVLSTQHSSEIDQ
26061	56429	A	26208	1	3771	
26062	56430	A	26209	239	451	LPPTAWMSTTNLTSAMLSVRG NVPMTLPARRRVNLPSSLICTCF HKPA*RI SMPKPWW*KARIISGN STS
26063	56431	A	26210	1	2079	
26064	56432	A	26211	1573	2562	
26065	56433	A	26212	275	643	SSRTALFTGSAVPGCAPPSGRSL FPQCLQSKLARSFPICRSRGAA ILFRRLSFSPTLILEDRIKRF MRENSRGPQVPAGLPMTTEEQL KKLGGRLRALGKLMPGEEES VLRIAERTNA

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26066	56434	A	26213	1	899	MGRTRRRDAAQAPGTRRSODS RGYPYVTRPEGTDADDPQKDK AALGSHRVAGQPELFSIDELTR RDPHSASGAWTARYTVSTIAAF ALVIANRLYTIEEEATTPSGCGP ASSSTSSRGVDMCLRLNLCMHG YDATIPLTLIAADSMDEYNKPD LSHVISQQRADDLTRQTAGEF AEQFNHLHFPQTWVTDIDAEAR VVKSQNNQWQYDKLVLATGA SAFVPPVPGREMLMLNSQOEY RACETQLRDARRVLIVGGGLIG SELAMDFCRAGKAVTLIDNAA SILASLMPPEVSSRLQHRITEM GVHLLLSQLQGLEKTDSGIQA TLDRQRNIEVDVIAATGLRPE TALARRAGLTINRGVCVDSYLQ TSNTDIYALGDCAEINGQRD*SS ARRVVPGRFPGAVRWQLPHP LRYCAGGPALPECQNPFPPAPV TEISTADERPSPTDAAASGCLLP VALTTPEYWQRCRLA
26067	56435	A	26214	1	1264	MDYMPVPGMDWLCRETAGM RVSIGKSSVFPNPELVMKV RQRSTIVTPSGFKAGAFNFERFK EASNQTLGSTFLYSLCPKNL GSQPLDFDTKKSYTLKVEAAN VHIDPRFSGRGPFKDATATVKIV VEDADEPPVFSSPTYLLEVHEN AALNSVIGQVTARDPDITSSPIR LYRIPGDDAKCVQFNREGVKA LKAKPVEKAAPAPAAAAAPKAA PTPAKPMGEQLALYRMAGSNA DRIQGRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPMTRTKELAEV VAAATPVKDKFKHPATRTFQA VRIWVNSELEKIEQALKSSLNV LAPGGRLSIISFHSLEDRIVKRF MRENSRGPQVPAGLPMTEEQ KKLGGRLRALGKLMPEEE/S VLRIARTNA
26068	56436	B	26215	64	663	
26069	56437	A	26216	27	791	
26070	56438	B	26217	1	1638	
26071	56439	A	26218	1	375	STKKQRGEIHHPDGHGIAQDRH LPRTSVDQRLRQTNNHAPGL*Q ANG*GVFKRCRAHSATT**KDD E*NESAENAA*GGKVEGTDVT GDLLHENPAITPDKCEHNQATD CQWVALSCGRHERSSV

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26072	56440	A	26219	213	407	TTCCCTNL SIPLANKYRSLSPQS DWRLSMPR*NRVYVQKAPARAN KTSPMKAPPANIALGVNVAR
26073	56441	A	26220	1	1179	
26074	56442	A	26221	176	569	WPMRHTFSEAHAAQRAGGKNP GHDTADYATNAVHTEDIAGIHH PQQA FEHGNAPQARQTSYHAD NQRAANPNVAAGWRHADQTG NRARTRPQQ*RLTTQRPFTEDP AKNCRRRCDHSIHKCCQCRDFIR RAR
26075	56443	A	26222	1442	2309	
26076	56444	A	26223	155	2929	HLHWVFVSGWFTVTRLAFGEG NNFFGNINWMLKNIETAYVM GSIYQYIHVAFQGSFACITVGLI VGALAEIRIRFSAVLIFVVVWLT LSYPIAHMVWGGGLLASHGAL DFAGGTVVHINAAIAGLVGAY LIGKRVGFGKEAFKPHNLPVVF TGTAILYIGWFGFNAGSAGTAN EIAALAFVNTVVATAAAILGWI FGEWALRGKPSLLGACSGAIAG LVGVTPACGYIGVGGALIGVV AGLAGLWGVTMLNAC
26077	56445	A	26224	2	1064	
26078	56446	A	26225	1849	2515	MEGHLWIRIDLSQSAVSHSVKE LENHTGVRLDRITREVVLTLD AGQQLALRLERLLDELNSTLRD TGRMGQQLSGKVRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQVVMESIRQGDVDFGIVI DPGPVGDLQCEAILSEPFLLCH RDSALAVEDYVPALPLPEGSP VVKRITPVVERQLMLVRRKNR SLSTAAEALWDVVRDQGNAL MAAA

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26079	56447	A	26226	102	1655	RKQMNYSLKQLKVFVTVAQEK SFSRAGERIGLSQSAV\SHSVKE LENHTGVRLLDRTTRAVVLT AGQPLALRLERLLDELNSTLRD TGRMGQQLSGKIVRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQVWMESIRQGDVDFGIVI DPGPVGDQLQCEAILSEPPFLLCH RDSALAVEDYVPWQALQGAKL VLQDYASGSRPLIDAAALRNGI QANIVQEIGHPATLFFMVAAGI GISILPALALPLPEGSPLVVKRIT PVVERQLMLINVIQTLRF AFIFR LSRRQHFAKVTPLLRRHGDYF VFIFDYG TANCSSVAVMRD GK PHLLKMENDSTLLPSMLCAPTR EACGRVDVIEVSKSKVRKNTY AMRYVAGQPAERILPPGSFASI GQALPPGEPLSTEERIRILVWNI YKQRAEWL SVLKNYGKDAH LVLLQEAQTTPELVQFATANYL AADHVPFVLPQHTSGVMTLS AAHPVYCCPLRERKPIRLAKS ALVTVPYIPFYLNS
26080	56448	A	26227	159	290	
26081	56449	A	26228	562	774	VLRMIT*SKSQFAQDMCRNVLL INNFGRIQHDP AIFHFQORNEAVP LWTVSAQEVKKDFTSGLRHGS VRGDL
26082	56450	A	26229	50	409	GYASQALILASIP AASRPSSARIS S*VPCGIKKSGRPFMFSTGTGLR WAISTSFTPLPAPPIMAFSSTVTS ASWLA AISRINASSSGFTKRIST SVAFSDSATFAASSTNSRNAPP VEM
26083	56451	A	26230	405	626	
26084	56452	A	26231	1	1528	
26085	56453	B	26232	1	1755	

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26086	56454	A	26233	152	2099	GNRLLVVSFIASFKNSTHFKGIF AMRIILLGAPGAGKGTQAQFIM EKYGIPQISTGDMRLRAAVKSGS ELGKQAKDIMDAGKLVTDELV IALVKERIAQEDCRNGFLLDGF PRTIPQADAMKEAGINGHYVLE FDVPDELJVDRIVGRRVHAPSG RVYHVKFNPFPKVEGKDDVTGE ELTRKDDQEEVTRKRLVEYH QMTAPLIGYYSKEAEAGNTKY AKVDGTFKPIYRGS LYSDQIG HTIVNPDGVVDCGRYGCLET VASLSALKKQARVWLKSPVS TQLDPEKLTAAQLIAAWQSGEP WITSWVDRSANAIGLSLYNFLN ILNINQIWLYGRSCAFGENWLN THIRQTGFNPFDRDEGPSVKATQ IGFGQLSRAQQGVLDGNMIITS GQIPVNPKTGEVPADVAAQAR QSLDNVKAIVEAAGLKVGDIV KTTVFVKDLNDFAPVNATYEA FFTEHNATFPARSCVEVARLPK DVKIEIAIAMLYTYGHYNDAP SAVRYPRGNASGVLETPLEKLP IGKGIVKRRGEKLAILNFGTLM PEAAKVAESLNATLVDMRFVK PLDEALILEMAASHEALVTVEE NAIMGAGSGVNEVMAHRKP VPVLNIGLPDFFIPQGTQEEMRA ELGLDAAGMEAKIKAWLA
26087	56455	A	26234	935	1020	
26088	56456	A	26235	145	373	

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26089	56457	A	26236	530	1865	RGNKRDLDMFKQSHASMYIKQ PEQLDYQLNLKEVITAVFISMV VLNISPSTLY/PDKPSPKDKYVAY AINIPDYELAADVYNINVTSPSG QQETFKILINLEHLRQTLERKSL TAVQKSQCEITPKKPGEAILHA FNATYQQIRENMSEFARCHYG YIQIPPVTTFRADGPEETPEEEKG YWFHAYQPEDLCTIHNPMDGL QDFIALVKDAKKFGVDIIPDYTF NFMGIGGGGKNDLDYPSADIRA KISKDIEDPVTKERKQIHPEDIH LTAKDFEASKDNISKDEWENLH ALKEKRLNGMPKTTPKSDQVI MLQNQYVREMRKYGVRGLRY DAAKHSKHEQIERSITPPLKNY NERVHNTNLFNPKYHKKAVM NYMEYLVTCQLDEQQMSSLLY ERDDLSAIDFSLLMKTIKAFSFG GDLQTLASKPGSTISSIPSERRILI
26090	56458	A	26237	14	2031	LIVLS*QHG/DLRQNRSGAEHFG LQRLMLHASQLSLTHPFTGEPL TIHAGLDDTWMQALSQFGWRG LLPENERVEFSAPSGQDGDPTL GLIKEVACELSGMMRRSQPWE EAESIPDRGESLLEVSGTPNAG WGAEGLAEREALLCCCCGPM GPDPLGLGSPGVRGRSRLIHH AISGEALWEVTSEGLDMAAAR QFAIEKGAPALRAMTFIERAAM LKAVAKHLLSEKERFYALSAQT GATRADS WVDIEGGIGTLFTYA SLGSRLEPDDTLWPEDELIPLSK EGGFAARHLLTSKSGVAVHINA FNFPWGMLEKLAPTWVGRNA SHHQTSYRDGPLTQAMEFEDK AQQRDVETARHFTFFRIANED KKTGFPRFQTIVITASHKTIDRT RYTYGAWRCYRPLLTVEEYRA TGSLITQPKFPPHKSSEVHRVPR NQGRFVAVNSTLPTEPATVAPV RNGNASRDTAKTQTAERPSTTR PARQQA VIEPKKQATVKTEPK PVAQTPKRTEPAAPVASTKAPA ATSTPAPKETATTPVQTASPA QTTATPAAGAKTAGNVGSLKS APSSHYTLQLSSSNYDNLNGW AKKENLKNVYVYETTRNGQP WYVLVSGVYASKEEAKAVST LPADVQAKNPWAKPLRQRHRD LRGDERRDDRRSEYFNQOVIS

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26091	56459	A	26238	732	1025	HEAKRTGRSYWFTAV*WLRG WRRMVARQNAKNCWHGTFFR VARVSLPISAHASSTHLGSAH YVPPSA YRNSRRYSRGLCRCRV SSCDAATGVVVVQ
26092	56460	A	26239	1905	3087	RVCSCDAGTLHWLQNLRCGLP VWCDGSGGTSGDPQQRGSEC TG*QSRSQ*MRPVQPS*RRPGV YGGLPDS\WLICVDRNKLEQLT PEKRRQAKLRAMKPDEFAQIQ QAVITQMLQHPQTLGEEASKLS KDFDRGNMRFDSRDKIYAQIKL VTPQKLADFFHQAVVEPQGM ILSQISGSQNGKAEYVHPEGWK VWENVSA LQQT MPLMSEKNEQ NL YDCGALFAPVTWTS GSAAF PRPLTVEELLVVTTEAA TAE RGRIRSN IHELRIACLRETTDNP LYERLLEEIDDKAQAQWLLL AERQMDEAAVFTIHSFCQRM NLNTNECCFQRTTKTIHRDSFK STPRAAKSCSGLLPALAPSQISS NTPIQLSRFKFSGVTSPTSAAAS
26093	56461	A	26240	1	2235	
26094	56462	A	26241	166	416	CHVVGPFRRVRRNLISAQHPLTL NSRHHTTTAARRLLRYFGTPR YRHSIDIHMLQDMTTSRLSSL RDQLHCRWLLPAERQAI

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26095	56463	A	26242	1	2084	MLFPLATSGAMEPPFFLAGTAG ALVGGGLQNGISGVLASLSAML QTGGQPGVVDNLNGIVDRAVLA AAGDADVASGAARLSARHRSI VISSMGERCCFIRSRITRICGHWI CPQGNEIPVVAVASHDTASAVI ASPLNGSRAAYLSSGTWSLMG FESQTPFTNDTALAANITNEGG AEGRYRVLKNIMGLWLLQRVL QEQQINDLPALISATQALPACRF IINPNDDRFINPETMCSEIQAAC RETAQPIPEDAELARCIFDSLA LLYADVLHELAQLRGEDFSQL HIVGGGCQNTLLNQLCADACGI RVIAGPVEASTLGNIGQLMTLD ELNNVDDFRQVVSTANLTTFT PNPDNSLYTTDKGALRMTTQL EQAWELAKQRFAAVGIDVEEA LRQLDRLPVMHWCWGDDVSG FENPEGSLTGGIQTGNYPGKR VMPVSYVPIWNSTLSLGSNWF NRKALGSPARYDVLPKWWRN VVKPTRTRYIGIAFYKVGEP KIEPDWMINGGVPELKKQLDL NDAVPEISGTLFREDYRNKPQT QQAADPPIRAKAAEIAVAHAH YLSIEFYRIVRIDPHAEFLSNEQ VERQLKSAMERWIINVLSAQIR PQPAVTHYRGLATVEMPVATG RYPTRYVGLVEPKTGRKHQ LRRHLAHLRHPIGDSKHGDLR QNRSGAEHFLGQRMER
26096	56464	A	26243	1	2871	
26097	56465	A	26244	690	824	
26098	56466	A	26245	950	1484	

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26099	56467	A	26246	1	2625	MVAFYRHAGRMWPGIALSCSL GNIAASILLFSTSSLNMTWTTINI VEAVVGAVLLRKLLPWYNPLQ NLADWLRLALGANSAGVNIS TATVCRQCEDAPCANVCPNGAI SRDKGFVHVMQERCIGCKTCV VACPYGAMEVVRPVIRNSGA GLNVRADKAEANKCDLCHNRE DGPACMAACPTHALICVDRNK LEQLSAEKRRRIPGNIRIRSGR YRRPVTAGCDVVSGRAGYAI HDGNNNSMAKNTSCGVQLRI GKVGQVGRPFVWLAQQLSH GSRMRDGTCLNKYDEYSRSGS MQYNPLGKTDLRVRLCLGCM TFGEPRGNHAWTLPEESSRPII KRALEGGINFDTANSYSDGSS EEIVGRALRDFARREDVVVATK VFHRVGDLPGLSRAQILRSIDD SLRRLGMDYVDILQIHRWDYN TPIEETLEALNDVVKAGKARYI GASSMHASQFAQALELQKHG WAQFVKSDENDAPDRQSGSTG SQCKNCGADTEPQVAAGPGLS ELNPVHCPLHYRAHFRADRH SVACSLDTPVTGHQVAPTYRQ QVPRAGQVHDPSKHTRMPCEN IDPVRTIIRISDPPVPASATLGA SKASRIRPRRSHIPEITAKSRKP GGQPKWQVICWLDREKVVV MQTVRDOIQGHVFTAHRLDRP TSGVLLMGLSSEAGRLLAQQFE
26100	56468	A	26247	1	1833	
26101	56469	A	26248	1	517	MRNKL SFDLQLSARKAAIAERI AAHKIARSKVSVFLMAMSAGV FMAIGFTFYLSVIADAPSSQALT HLVGGLCFTLGFILLAVCGTSLF TSSVMTVMMAKSRGVISWRTWL INALLVACGNLAGIACFSLLIWF SGLVMSENAMWGVAVYTAPR AKCIIHLLNLSASALCAI
26102	56470	A	26249	3117	3527	EAVHRLARYRDAPRRS**SPLL CASVYP*LEQVPLQAQAVVPLR VLQAGKPVVPVAVLNAQAAAL ARPVAKLAAATAVQAAADRQ AAAPALDAEHVAAPALQAA AGPVDAAAQTHKAVGTGVAA TDEQHPAPER

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26103	56471	A	26250	2	563	STTSITAFSATTAGTPTSGNTP SASPIWRRPNFWARKVYLLHW FCHRQPSKEVLFHLALYRNNPR CKAVVHLHSTWSTALSCLQGL DSSNVIRPFTPYVVMRMGNVPL VPYYRPGDKRIAQDLAERETH/ NHAFLLANHGPPVCGESLQEA ANNMEELEETAKLIFILGDRPIR YLTAGEIAELRS
26104	56472	A	26251	2	1481	PENQINKLKQAIADYRSHQKC VNQPSPTITPRLFAITVITDERG YATGSAGNLSL/LLPDGNLLAT PT/GSCLGN/LDPQRFSKVAADG EWL/SGDKPSK/EVLFHLALYR/ NNPRCKAVVHL/HSTWST/ALS CLQGLDSSNVIRPFTPYVVMR MGNVPLDLAELAA/DNQAFLL ANHGPVVCGE/SLQEAANNME ELEETAK/LIFILGDRPIRYLTAG VCP/LAKMLNGTGQYLSIKRCT NNRSVRGTCSAPRAGPKGYGL MMMIDVLSASYSAYRSGDRTL LYSYHRASACADSTTLTVLISY TFHLVNSYSTVPPLESGTQPA SPSFPTRVSDDHNRDFFLLSPC GLLQNLAQCIQVGIQLDFGCV IISAQTETDGPLVCGRFEEGTPF SPQTPRDCDPNRSYSGNTQGVR GATSSPGSAISFEQTVNARSHVL RVTLTLGLTRPMLVYTGSLKWI NICILPISLKPLRYYIHLAAQFPT APISLGRSLHVVVPHEEVAM
26105	56473	A	26252	1	413	
26106	56474	A	26253	3	247	
26107	56475	A	26254	300	665	
26108	56476	A	26255	1	1854	
26109	56477	A	26256	1	1611	
26110	56478	A	26257	942	1040	

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26111	56479	A	26258	1616	3678	PLAKTGRQREQLAGLAK/AHPS LTLHQDPVYVTRADAPVAGKV ALLSGGGTEHEPMHCGYIGQG MLSGACPGEIFTSPTPKIFECA MQVDGGEGVLLIHKNYTGDIIN FETATELHDSGVKVTIVVIDD DVAVKDSLTYTAGRRGVANTVL IEKLVGAAERGDSDLACAEELG RKLNNQGHSGIALGACTVRSR GKPSFTLADNEMFEGVGIHAIL KGDIPAEAILASIKPAGVVSRA DVLVLPNQFQALRKSFIPERPVP VMVIRLFELPVQISLGVYSLER PANPQPIAYLVLPQRRKANNQN ASTSAIIRATIGEPISCSVPSRGC EGGISVAETVPAMIIAIGITISEG LDARYRHVNSEHDPDRQAKF EWRYFGNLGKTVNDWRKNNK ADIKEDGNRRCRHTNQPHCRIE AVEYDDGRLCPLHGAHRGQSS DGELVKPTVKQSLAVHYSIGK LRHRPNHGAVVYQRLRSGMGL MNAFDSQTEDSSPAIGNRLRSR LARKKLESEMVEEELEQMIRRE FGEQEQLPSERELMAFFNVGRL RAGSVKTRQSGANKQRRTRCV SRPSADTIIGELSGMAKDFLSHP GGIAHFEQLRFFESSLVRYAA EHATDSRDPYRYPKFYSISRVP VSDNITLQQLLSLNDQPARCK PSARCRLHGSHTSRYEENHRHG
26112	56480	A	26259	185	775	IPEIFSGETHLKVSTLSKPTFSISS LIRCTTRFSSQLSLGIATMSHRK RVISALKSLSRLSANSLVFANQ VERSSLTNLGCTRCSG*SLFWQ RPALR*PFGLCPTVALTLYLVSP EW*KAVSVKCRNRRLTLMTS PICTNSGTLTTAPVDRVAQVTF QSPECLQHMRLTIALRYFRVAL SRRLLVYASVCFTFSG

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26113	56481	A	26260	301	1313	RLEHDDGVCLHRANHRYPGCRLLHI.DYVEPQLQHDDALRAAVMMFKQYLQVTKPGIIFGNLISVIGILLASKGSIDYPLVIYTLVGVS LVVASGCVFNYYIDRIDRKMERTKNRVLVKGLISPAVSLVYATLLGIAGFMLLWFGANPLACWLGVMGFVVVYGVVSYLYMKRHSVYGTLIGSLSGAAPVIGYCAVTGEFDSNAAILLAIFSLWQMPHSYAIAIFRFKDYQAANIPVLPVVKGISVAKNHITLYIAFAVATLMLSLGGYAGYKYLVAASVSWWGLMALRGYKVADDRJWAAQSCSGFSIIPITALSVMMSVDFMVPDSHTLLAAVW
26114	56482	A	26261	3631	4078	CFLNFKTLLVHLFRVRFLRLRHRKLHPVGLGGPVNKAAYAFCLGAMANGVYGPYAFASVKMVSATFTVASTMLAPRWLLGLAGITEGAIPMAIEDPLRVIGSFVLGSMVTGAIVGAMNINRTL.RVEASVTSAQIVQTIIRLRR
26115	56483	A	26262	814	2126	CTGCRKQRLPVVQGFAGLAA NMIGSGFLGAVVGGIAGYLMRWVKNHLRLSSKFNGFLTFFLYPVLGTLGAGSLMLFVVGEPAWINNSLTAWNLGSLGSNALLGAILGFMCDFLGGPVNKAAYAFCLGAMANGVYGPYAFASVKMVSATFTVASTMLAPRLFKEFEIETGESTLLGLADITEGAIPMAIEDPLRVIGSFVLGSMVTGAIVGAMNIGLSTPGAGIFSLFLLHDNGAGGVMAAIGWFGAALVGAASEGKRIFRYRDLIIVNSNQLFLHDHFRFPRWEGLESVFLLAAEQQDVGIWPPGLGAM.LGLATAVVLGFLLYWGGIRLNLGAFFKWTSLFILFVAAGLAAAGAIRAFHEAGLWNHFQEIADFMSAVLSTHSLFGTLMGIFGYQEAAPSVSEVAVWFIYILPALVAFALPPRAGATAS
26116	56484	A	26263	1	525	
26117	56485	A	26264	1	700	
26118	56486	A	26265	1	1428	
26119	56487	A	26266	254	475	RDQLVSELNQMLV*KSAFRMALITSRWPMVTHWFREVRRGNWRQFLPALTLVRLSLMLMGRQAILRSRRNY

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26120	56488	A	26267	1	1657	MLIQRRRLAFDRAKHRRRAEML AQRARGEIEAHHHSSPEGAIEV DESEVDLDAISAQSLRLVRSILM LIALLSVIVLWSEHSAGFLENI SLWDVTSTVQGVESLEPITLGA VLIAILVFHITTLVLRNLPALLEL AILQHLDLTPGTGYAITTITKYL LMLIGGLVGFSMIGIEWSKLQW LVAALGVGLGFGLEIFANFIS GLIILFEKPIRGDTVITRDLTGS VTKINIRCHTHRRQQLLQQA ATSSADVIYLGAEVCSKRRATK VGDWLEMAKSLAGSGKQIVLS TLALVQASSELGELKRYVENGE FLIEASDLGVVNMCAERKLPFV AGHALNCYNAPLKILLKQGM MRWCMPVELSRAWLVNLLNQ CDELGIRNQFEVEVLSYGHLLPL AYSARCFARSEDPRPKDECETC CIKYPNGRNVLSQENQVVFVFN GIQTMSGYVYVNLGNELASMQG LVDVVRSLSPQGTDTFAMLDAP RVNENGAAPLPLTANSDCNGY WRRLAGLSLRQIKTCLIFLLCQP RGRRPYRTRAMPPLTMPANSP
26121	56489	A	26268	482	605	
26122	56490	A	26269	1	298	MWPGMVTHAVRIPLHNDTVTL SDNFQPFAGTDAMTITRPLEML RDGKCPQPDWISSEGACAGNA TDSPPHFELKAGKTITLEDGRQI NGADYLAAPVPGKALAIFGDT GPCDAALDLAKGVDVMVHEA TLIDITMEAKANSRGHSSTRQAA TRESELFRYTVKHSILFASVIGII TLLQASTKIYTPGRKEQGEPM PRRTPARF*IKSGQNNHAGRWK AD*RRRLSCSSAR

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26123	56491	A	26270	1	1707	MTRDGLANKALAVARTLADSP EIRQGLQKKPQESGIAIAEAVR KRNDLLFVVTDMQSLRYSHPE AQRIGQPFKGGDILKALNGEEN VAINRGFLAQAALRVFTPIYDEN HKQIGVINDSRWSIHSVLFMG LVGLIGTCLVKVKKILFGLPE YEISTLFEQRQAMLQSIKEGVV AVDDRGEVTLINDAAQELLNY RKSQDDEKLSTLSHSWSQVVD VSEVLRDGTTPRRDEEITIKDRLL LINTVPVRSNGVHGAISTFRDKT EVRKLMQRLDGLV/NLC*RTS* TIPLRAHSPQSKSAIYHEIAP*NA PAFYRRKCHCADIFLPYF*TCR\ RDRAMSAYLRYIVQKADSSFL YDKYQNNQSIAAHVMRALAAEQ SEVSPEQRRAICEAFESANNTH GLNLTAHKYPGLRGTLQTAST DCDITVEAAALLPAFDQAVEGN RHQDDYGSGLGMAEEKFHYYL DLFRAVGDGHNSKEDATFGLG WRVNGNATMTPTFGTLASPQT YGHGTWGTGTVIDPVNHMTI VMLSNKPSPVADPQKNPNMF ESGQLPIATYGVVVVDQVYAAL
26124	56492	A	26271	257	817	TSSRCISLRTSVLSLKVEMAPMI TPLRLTGTVLISNSRLIVISSR RGVPSRNTSETSTTCDEWLSV DSFSIVLRLTVIQQFLCGIVDQR DLAAIVHGNDAFFRLQHGLA LLKQRGDFVGFQAEKDFQYL NQNAGANQSDQHAK*Y/LTR*C SSDCH*SVGSHGLTQGRSPPRQ FVYDFHRRWG
26125	56493	A	26272	I	2700	

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26126	56494	A	26273	1	1038	MGCLDLGDGRAGSVARYFRRY RPPCDAALDLAKGVDMVHEA TLDTMEAKANSRGHSSTRQVL KKILFGLEPYEISTLFEQRQAML QSIKERSRRHRLPKEKIMTPTI ELICGHRISIRHFTDEPISEAQRE AINSARATSSSSFLQCSSIIRITD KALREELVTLTGGQKHVAQAA EFWVFCADFNRLHQLICPDAQLG LAEQLLLGVVD TAMMAQNALI AAESLGLGGVYIGALRNIEAV TKLLKL PQHVLPLFGLCLGWPA DNPDLPKRLPASILVHENSYP LDKAAALAYDEQLAEYYLTRG SNRRDTSWDHIRTIIKESRPFI LDYLHKQGWATR
26127	56495	A	26274	1	1338	
26128	56496	A	26275	2	375	HSDPEASGLTRLRAMEQRRTV DFFARRRTPGSVPTDRR*TIIVR MIPCTSSGRRTKAMVILRTSLV NPASNE/CATELFNALDVSIQNP RMIIIS*IQHRTLSGSLVAVG RMCSTLTPRVIFEH
26129	56497	A	26276	219	767	RFTQGGKPINNPAVIRPLDFPQN GSRPLANQIFTSLKVGDFYFGK RHKDVLRAIRNLKCSDDFTQRN FAPIDFIDKNGDVQPMYNITRD GCMMLVMGFTGKTA AAVKEC YNAFNWM/AEQLNRRMAMGE ELQHRYAIKETRSKLKGTIG/IR LMNERKKEKRVLELEHEHIMQ VTQPELLIG
26130	56498	A	26277	16	104	HICQSAPL*RGSSGLNGYGQYR PAGFLDG
26131	56499	A	26278	3	399	
26132	56500	A	26279	1112	1831	TGIRNCAPLSLTWKSCTANKV RCGHIRYPLADGAKTSDGKDY LVVATTRPETLLGDTGRSRLTR KIRVTKELIGKYVILPAGTAPGV RQGPVWMPGDEVKVTCKNG VVNEIWTRNHADIPLRPFVAVL ASGSFFSVGLVAERNIGIREPILG LDVLQTATRGWEYKGDFFAPQ PWQQFGVTTDET/LRPSQAGQT IENLFAIGSVLGGFDPIAQCGCG GVCAVSALHAAQQAQIRAGGQ
26133	56501	A	26280	3	790	
26134	56502	A	26281	334	609	

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26135	56503	A	26282	1	1338	MTRHYGAEATNALLPGKASKH QIVGCGVNALSDLDPRRPDKTR SVASGIGAALLRLIKTLADDL QNLTDLSVFNGERYKDAQHV IRAAGEKNQAFIAGARHDLGGE LGVLGVWIPASKVNGIMGPSVP WLTFRVSNIAGESAEGLLVTKP KNYDQVPANKPIVDAIKAKKQ DPSGAFVWTTYAALQSLQAGL NQSDDPAEIAKYLKANSVDTV MGPLTWDEKGDCLKGFEGVFD WHANGTATDAKRYCANVKGV NPDTQEPSPSGVKVNPKVDER LIRQEAGMVQQFYLFPHLTAL ENVMFGPLRVRGANKEEAEL ARELLAKVGLAERAHHPSELS GGQQQRVAIARALAVKPKMM LFDPTSALDPELRHEVLKVMQ DLAEEGTMVIVTHEIGFAEKV RSRLIFIDKGRIEDGNPQVLK NPPSQRLEFLQHV
26136	56504	A	26283	1170	1575	DPPVLVQRDANSTVRFPHASAS ADPAGDIPPIFAQAAGADLVY VGVEPPKPKAEVILVAEYSPKPT VADLGCPHVKVSRYPPEFTQ VITPVQCYVTIDALGQYAAWT RANMTYRPGSNIIQNLGNDIRL RTVQ
26137	56505	A	26284	3	1351	RTAPETPNQRPATLDSGILGGYI APDNLTTTFGGHSLFDERFCLA HRCQKAAEDDAFPHDSLDAAS LLEYAREKLNGLDVEVYHWN QNFAPELDLYARFDSALKTFT EQLQQADGLIVATPVYKAAYS GALKTLDDLPERALQGVVLP LATGGTVAHLLAVDYALKPVL SALKAQEILHGVFADDSQVIDY HHRPQFTPNLQTRLDTALETFW QALHRRDVQVPDLLSLRAPKP KAEVILVAENSPIKTVADLKGH K/VAFQKGS/SSHNLLRLA/LRQ AGLKFTDIQPTYLTPADARAFAF QQGNVDAWAIWDPYYSAALL QGGVRVLKDGTDLNLQTSFYL AARPYAEKNAGFIQGVIAFSE ADALTRSQREQSIALLAKTMGL PAPVIASYLDRHPPTTIKPVNAE VAALQQQTADLFYENKLVKK VDIRQRIWQPTQLEGQL

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26138	56506	A	26285	364	1937	KLSGRHCTAAMFRFLTFCLEGM MPMRNIKLALAGLLSVSTFAD AAESSPEALRIGYQKGSIGMVL AKSHQLLEKRYPEKISWVEFP AGPQMLEALNVGSIDLSTGSDI PPIFAQAAGADLVYVGVEPPKP KAERILVAENSPKTRTDLKGH KGAFQKGFSSHNLLRALRQA\ GLKFTD\NPTYLEPRWRPRAA\ FQTRGTVD\AWIWDPPYSAA LLQGGVRLVKDGTDLNQTGSF YLAARPYAEKNAGFIQGVLATF SEADALTRSQREQSIALAKTM GLPAPVIASYLDRHPPTTIKPVN AEVAALQQQTADLFYENRLHY SEYCRPMVSVGNWFLDGSHSV FSYDALDRLVQGGFDGRTQR YHYDLTGKLTQKQWQYDGHG WLTDISHLEGHVAVHYGYD DKGRLTGECQTVENPETGELL WQHETKHAYNEQGLANRVTP DSLPPVEWLTYGSGYLKAGMKL GGTPLVEYTRDRLHRETIVRSFG SMAGSNAA YEMTSGETLIDLC
26139	56507	A	26286	511	1152	SVRFNIVFHFMRLLRFCCVLDH LICFTSPVNTFLRYNAFTLCNGE FGMSPALQTLRALRYCKEIPA LDPQLLDWLLLEDSTMTRKFEQ QGKTVSVTMIREGFVEQNEIPE ELPLLKESRYWLREILVLCADG EPRLAG\RTVPVSTLSGPALAL QKLGK\TPLGRYLFSTSTLTRDFI EIGRDAGLWGRSRLRLSGKPL LLTELFLPASPLY
26140	56508	B	26287	184	415	
26141	56509	A	26288	15	87	
26142	56510	A	26289	78	157	CKRYGKARDTG*QPRTQKCTC CELDE

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26143	56511	A	26290	1	1817	MTSAISLGSRCSGRIPSDIHSNL DITAFNWQPDLLTIWHRQLHLH LTRLGGGHFYRQEVHLWRD KSGDKRRPQGDPKTTGITAKVI NVRSTKLVLPHRITATRWKR KRSRMLHTNTGKLVFNRRDQK RCTRKVMFDKALKLLDEAERL GSTSARSTIYQQCKRQGVITPHS ADFATTVRLLAHLSSQERLGLKQ DSIYISLTDHCQFAIKRFQQNVL LPNPLLWDIQLRYPKEFQLGEE ALTIIDKRLGVQLPKDEVGFIA MHLVSAQMSGNMEDVAGVTQ LMREMLQLIKFQFSLNYQEESL SYQRLVPHLKFLSWRILEHASI NDSDESLLQAVKQNYPPQAWQ CAERIAIFIGLQYQQLGLTPQAV SKIINDIEDYFGVELVVRKNTG VLTTPAGQLLSRSESITREMK NMVNEISGEKNPGESEKELET VYVQAVGAHWEGNQVWLILA GGALFAAWPRVYAAAFSGFYV AMILVLCSLFRPLAFDYRGKIA DARWRKMWDAGLVIGSLVPPV VFGIAFGNLLLGVPFAFTPQLR VEYLGFSFWQLLTPFPLLCGLLS LGMVILQGGVWLQLKTVGVIIH LRSRVRIPCDLHIYAQMA
26144	56512	A	26291	557	808	
26145	56513	A	26292	8	274	
26146	56514	A	26293	523	1851	
26147	56515	A	26294	1	589	

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26148	56516	A	26295	1	1848	MDLSTPERGSPYPRLLPCGDPL GETIVAIDQEAKPSTEDLGNKK ETKYIKLVIRWDNSDFNFLYS NYERIRARTTKKEDSATNPVT FEKHGSHAVVYARRSATVLT RNKEAPRVPPGGYMYSFVDIPE ALTQGETVAEAMEAAKDALLT AFDFYFEDNELIPLSPNLNSHDH FIEVPLSVASKVLLNNAFLQSEI TQQELARRIGKPKQETRLFNH HATKIDAVQLAAKALGKELSLE CLMDILNLNKHISGQFNAELES RTQVMTLGGMVDKQLSDAITA IHNQSDLAKRVIIEGHKNLNM MEVAIDEAR/C*AIIAKHQSTAS DLRLVMVI/SKTIAEMERIGDV GRNKICRTALEKLSQQHQP*VV SLES/SLDRHTIQMLHDVVKAF RMDIDETAKCQIFVEYVLKPKV IWLLCFANIFYVVRIGIDQWST VYAFQELKLFKAVAIQGTFLFE AGALVGTLLWGWSLDAANGR RGLVACIALALIIATLGVYQHA SNEYIYLASLALGFLVFGPQLL IGVAAGVFPKKAIGAADGIKG TFAYLIGDSFAKLGLGMIADGT PVFGLTGWAGTFAALDIAAIGC ICLMAIVAVMEERKSAARKKFS
26149	56517	A	26296	395	1428	TSATATSTFALPRGGGYLVVSE WVVLRFTHDIFLRIFPCDNGRTILI RFGIFRMLMIVAIETQQFPVTAI FRVIGMVVINVNASEETNRRL HHRSLRLIQECVMDSLNLNKH SGQFNAELESIRTOVMTMGGM VEQQLSDAITAMHNQSDSLAK RVIEGDKNVNMEVAIDEACV RIIAKRQPTASDLRLVMVISKTI AELERIGDVADKICRTALEKFS QQHQPLLVSLES/GRHTIQMLH DVLDAFPRMDIDEAVRIYREDK KVDHVEYE/GIVRQLMTYMMED SRTIPSVLTALFCARSIERIGDRC QNICEFIFYVKQDFRHHVGGD ELDKLLAGKDSK
26150	56518	A	26297	667	1002	
26151	56519	B	26298	1	1716	

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26152	56520	A	26299	1001	2193	LMAATKPAFNPPGKKGDIFSV LVKLAALIVLLMLGGIIVSLIIS WPSIQKFGLAFLWTKWDAPN DIYGALVPIYGTLTVSFIALLIA VPVSFGIALFTELAPGWLKRP LGIAIELLAAIPSVYGMWGLFIF APLFAVYFQEPVGNIMSNIPVG ALFSGPAFGIGILAAGVILAIMI PYIAAVMRDVFEQTPVMMKES AYGIGCTTWEVIWRIVLPFTKN GVIGGIMLGLGRALGETMAVTF IIGNTYQLDSASLYMPGNSITSA LANEFAEAEESGLHVAALMELG LILFVITFIVLAASKFMIMRRIA LTLSMATMAFGLFWLIWLMST ITRGIDGMSLALFTEMTPPPNT GGGLANALAGSGLLILWATVY CGPLSDDRGGRPTI
26153	56521	A	26300	1	1645	MPAFPPYADYFSGLTATTAALA ALHKVRETGKGESIDIAMYEY MLRMGQYFMMDYFNGGEMCP RMSKGGKDPYYAGCGLYQCAD GLLSLDCVHRRLLGAIDPILNECF KDIGLAHLGTPEIPEGTQLIHRI ECPYGPLVEEKLDAWLATHTIA EVKERFAELNIAKAKVLTVP ESNPQYVARESITQWQTM DGR TCKGPNIMPFKNNPGQIWRG MPSHGMDTAAILKNIGYSENDI QELRPNNKRTKMDRGAMDII GGQHLRQMWDLDADVYGHKT ALICSSGGVVNRYSYLELNQEI NRTANLFYTLGIRKGDKVALHL DNCPEFIFCWFLAKIGAIMHE AVIALASPDNMNAFELTP*SGK LITTFPHLPLAISA*ASPACSEK RWMALRGHSFQSVRSWAHFS IWNRLVTQEPIRR

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26154	56522	A	26301	2	1021	TPGNNVDSIFLAFFLNQFLTGLY IMGKTISIKVLFGIYLLMAAKV FAFSCNVGGINGAGTTSVYV NLDPVIQPGQNLGVDLAHHISC WNGDGGWYDTHMNLVQGS AFAGSLQSYIGSLYWNNTYYP PLTTNTNVLIDIGDKTPMLPFK LYITPVGAAGGVVIKAGEVIARI DMYKIATLGSNPSNFTWNIIT NNNAVMPITGGCTVDSRNVTD LPDFPGSAEPLGVYCSSEQKLS FYLSGATTDSRQVFANTAPDA TKASGVGVTLMQRQLAGINDS HLLHYLDDEVWDNDYLATPHF LLKSAILRSMNDALMTRVTGE KNGQVRLIEIER
26155	56523	A	26302	522	714	
26156	56524	A	26303	1	976	STCSSRSHLHLIQASPIPNVYA TAVAARIIADVQGISDTCVIAQP SPHPGALRTLVTTFDEPETPQP PGAAGFQLVQKKQVQLHNVLV VMTPHAFAGQTVIITLPGEQQT LSVAPLKNVQVLVTQQLHLRDR LWWPGAFLLDFAAKVKALKD/ YPNHVMAQRASGEAEADDDV AATIKSVRQQLNLNITGRPLV KLDPDFVRVDENSNPLVGDYIT LYTVQRPQTEQGSFKVKRARA RVRQTRAPLFGPKSPAPEHMES ELEFELIGPSKSTSGNPRGLRSE RPVLFCLYPEMPTAAARAILIAE EQSREVKIALVVLDRLQRE
26157	56525	A	26304	1	1701	
26158	56526	A	26305	1839	2038	ARSGCFVRQSCPRGRCSKNRR WRDPYDHYPARPAYCP**R/WC M*LSTLATPKKVSCKPAPAAH RWR
26159	56527	A	26306	1	3270	
26160	56528	A	26307	1962	2049	
26161	56529	A	26308	94	942	
26162	56530	A	26309	1	4104	
26163	56531	A	26310	879	1367	TASELGKSCSRDHTPCTASVRA LYYARLRHAPANDPGEDGWAL AAKPPALPPRNSLSQAIIFRDKP NLPHRSPATYRQTERG*DTRSE FHA*TDIAPVATRARAGEFCRQ MFWGEDQADEQPA**ACCHRK *PVPK*DLAMLRAPPRMDSPPD ASRTSDLHN

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26164	56532	A	26311	1203	1911	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDHK RPREALLDSLKKLQLDYIDL LHAWNPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQG GKGVFQDKVIRDLADKYGKTP AQIVIRWHLDSGLVVIKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDQDQFGG
26165	56533	A	26312	3	793	
26166	56534	A	26313	181	336	
26167	56535	B	26314	1	374	
26168	56536	A	26315	591	679	
26169	56537	A	26316	937	1395	YRLAAGSCGIRRRNRHCQRRPG RNSKRLIALISAIGMSIFLQNYV SLTEGSRDVPASSVPLTPASLLI AGSPPH*TISRLSGPLLREIMLK QLYHCGKSLTNLPREILRM*G* LTGEEIELARGDFHIDIWHRA VTNTAHKTGITQAQHRH
26170	56538	A	26317	627	878	VVEWFEPLICVNGWESKWPVL LSE**PETVGTNCDSSN*IPASLN TSYTGMLMAFDAMVAVPTS*TC KIRRRVAGTKCGNPRA
26171	56539	A	26318	125	3078	IYTVIEIQLGFAFVTGENTTGIN SGTISLLQNGKDPAPSPVILLAT NGGSATNAGTITGKVTEQHSVF NKYSTGTSSNFIFNNDVSSITGL VAQNSNTIINTDSGIIDLYGRGS VGMLAIADSTAENQKGITLDSM WVDANDTTAMRDIASNSAIDF GTGVGVGTDRYRGRGRKNAPAF NQLGGVITINYAGAGMAAYG ASNTVINQGTINLEKNGNYDDS LAANTLVGMAVYEHGTAINDQ TGVININVTGQQA
26172	56540	A	26319	205	419	
26173	56541	A	26320	1829	2903	AWKVSHCAARPSFSRRWRGEK CTAGRRSQQFSARSTLKPMPSP R*SSMHR**MPSASCALRLPIP PAAAQSSHQSKKLRITSDNASPV AAARPVRPIRWT

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26174	56542	A	26321	402	1781	QRTTGAERYVPHIQCPCPASSL SAGPRGLHPAKVQEGVDIAIEN DVIVAIGDALTRQYPDA SFKEM HGRIVMPGIVCSHNFYSGLSR GIMANIAPCPDFISTLKNLWWR LDRALDEESLYYSGLICSLAIAIK SGCTSVIDHHASPAYIGGSLSTL RDAFLKVGLRAMTCFETTDNRN NGIKELQEGVEENIRFARLIDEA KKATSEPYLVEAHIGAHAPFTV PDAGLEMLREAVKATGRGLHI HAAEDLYDVSYSHHWYGKDL LARLAQFDLIDSKTLVAHGLYL SKDDITLLNQDRAFLVHNARSN MNNHVGYNHHLSDIRNLALGT DGIGSDMFEEMKFAFFKHRDA GGPLWPDSFAKALTNGNELMS RNFGAKFGLLEAGYKADLTICD YNSPTLLADNIAGHIAFGMG GSVHSMVMNVGMVYEDRQFN FDCSIYAQARKAAASMWRRM
26175	56543	A	26322	284	340	
26176	56544	A	26323	113	646	WTLVPWNWNTQPYLGLFF*FIR DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQRSDSSLR EKKITKHHTKRTASLILHAMI CCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT EQ
26177	56545	A	26324	1	582	
26178	56546	A	26325	3	947	QTQEWSGSATFTSDGKIRLFYT DYSKGHYGKQSLTTAQVNVSK SDDTLKINGVEDHKITFDGDGK TYQNVQQFIDEGNYTSGDNHT LRDPHYVEDKGHKYLVFEANT GTENGYYQGEESLFNKAYYGGG TNFFRKESQKLQSQAKRDAEL ANGALGIIHLLNNDYTLKKVMKP LITSNTVTDEIRANVFKMNGK WYLFDTDSRGSKMTIDGGATQA FAKENNQKAYKETYGVSHTIR HDMLQIPKQQQNEKYQVPQFD QSTIKNIESAKGLDVWDSWPLQ NADGTVAEYNGYHVVFALAGS PKDA/G*HINLHVLK

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26179	56547	A	26326	2	223	RIPKINIESAKGLDVWDSWPLQ NADRTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNISID SWKNAGRNVFKDSDKFDANDPI LKDQTQEWWSGSATFTSDGKIRL FYTDYSGKHGKQSLTTAQVN VSKSDDTLKINGVEDHKTIFDG DGKTYQNVQGFIDEQNYTSGD NHTLRDPHYVEDKGHKYLVE ANTGTENGYGGEESLFNKAYY GGGTNFFRGATQAFAKENNQK AYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQADGTVAE YNGYHVVFALAGSPKDA/G*HI NLHVLSKGRRLNRQLEKRG
26180	56548	A	26327	1	803	MLEDPRKGLTSPVSHNLHFQ FHLGPLLPGSPMKKWPAVLT GSKSPKLESYKHFQKIWDMHG EPSKREEGAGLTVNQHIPNGAS TCNEGPQRLEALGARIPMAAGF SSSKPTLVTPRRAYRADLRLEG YWGCGQVPGPLVAQGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDA/G*HINLVLSKGRRL NRQLEKRG
26181	56549	A	26328	2	439	
26182	56550	A	26329	1	1084	MVIAAMETQLSNGPTCNNTAN GPTTINNCSPPVDSGNTEDSK TNLIVNLYPQNMTQEELKSLFG SIGEIESCKLVRDKITGGATQAF AKENNQKAYKETYGVSHITR HDMLQIPKQQQNEKYQCDNLKT CHTSHGSMVMAETAVINHKRRK NSPRIVQSNDLTEAAYSLSRDQ KRMLYLFVDQIRKSDGTQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIRKGTQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTPERR**HINLVLSKGR RLNRQLEKRG

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26183	56551	A	26330	34	1949	MGYLNNAVGYREDLLANRAIV KHGNFALLTPDGVVVKNIIPGYE NCDATILSTPKLGASFVDYLV LHQNGGNQQQFGVEGIEFRY VISGNITAKAEGKTYALSEG LYCPPGSLMTFVNAQAEDSQIF LYKRRYVPVEGYAPWLVS SELERIHYEGMDDVILLDFLPKE LGFDMMMHILSFAPGANHGYIE THVQAEHGGATQAFAKENNHK AYKDTYGVSHITRHDMLQIPKQ QQYEKYQDTHDTPYCEPLPET RLWGD TDVIGLFD AETDMNDV VAILENHPLLGAGFAHKIEQLE DKDWEREWMDNFHMRFG LWICPSWRDVPDENAVNVMLD PGLAFGTGTIQLSV PAMLDSS THTRMRSTLNLYEITRMSTVS TSEHSMYTLVQVDMKEAQKP DTASYRTFNEFFVRPLRDEVRPI DTPDNVLVMPADGVISQLGKIE EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRD YHRVHMP CN GILREMIYVPGD LFSVNHLTAQNVPNLFARNERV ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDES FVVG GPVG DFELLCHGTVCVVGKMRDLIL QLSKSSIYSTKPPSRQVSVMLC
26184	56552	A	26331	1	145	LRLGLLYGRRFVPPP*YALLNK DSSPWYFSPVPLASKTRYLWL LSPT
26185	56553	B	26332	1	3090	
26186	56554	A	26333	3	832	
26187	56555	A	26334	1	3258	

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26188	56556	A	26335	184	2324	ENRVRLFVLIVFQDLPTCYVNH NFCVCTAADTFTTITPKAGDAR LIGIAQTVRHLEDPMRWAKSIH KSCEILDPHRAVPKENTHPARK INISDPAAGAVARIRYEGVLSVC RASASAYVSRSTITVACWYVS NTGVTGATIGVKRQHRHARLFS GDGAPGFGTGKRDIRQLRLVR IQIQRTFFAAVLHVPTPWSRAID AAALLTVIDVKVLTACACQAC RTLALRVAQVIDRCSNPGDIMS SVARRYWFISWSAKRDCAVS YDQDPGQAQRSCRSCLVAVDR GLWLSAYCRSLMTQTLLPDDV PRILPNASSPSRLRCLQHLGNRY LLDLRKLWLHRSQFSLCGWEK RLVKDLTRIQDTGRAKEILGAT ATLEFRLVNTNVQAAAASGR VPGDSEVKQREGQPVVLYKR VILTGDHITDSTSSQDEYNQPO VNISLDSAGGNIMSNFTKDNIG KPMATLFEVEYKDSGKKDANG RAVLVKQEEVHIANIQSRLGNS FRITGINNPNEARQLSLLRAGA LIAPIQIVEERTIGPTLGMQNIQ GLEACLAGLLVSILFMIIFYKKF GLIATSALIANLILVIGIMSLPG ATLSMPGIAGIVLTLAVAVDAN VLINERIKEELSNGRTVQQAIDE GYRGAFSSIFDANITTLIKVIILY AVGTGAIKGFAITTGIGVATSM FTAIVGTRAIYNLLYGGKRVKK
26189	56557	A	26336	1	369	

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26190	56558	A	26337	1	1316	MNGLLSDSDLSLSSCQQRVKA RLHEILQKDRDFTAEDYEKVES RIYHFARLSVGGYTTADSSLTK VYLQLMKAPKKRRGEVNVGT VVAFIKGGFPVVKDYFRPAA DGSSALCRFFPTGNVHDQSDPQ KVTGDGAVVPVQPTDGPGLRCL RRARGCGAGRQGREQAQDCG AEIQAEAAASRASRVQEGSYPRP PNGPFSTDLTGLMQFTKLLVLK VESQLTRRIRKCHNLREANIREE LRFNCTNVALRTGVQFNRRPD SPGYSRGVLSPERHVRTRLTYFT SESHVHSLLSILRYGALCNRGG TLCCRAIHTLRHTIVLVNGVTY TLNLVQLTFYGNVSEIIRHQCC LTRHGNHPLPLTAIQGIALFSDN QAAYRFRADQRTLRFGLPVAR QPVRRGGFHDIVIVDFGTARQ QQE/LRLQLRVFSSFVLHEKKR
26191	56559	A	26338	2	1415	
26192	56560	A	26339	1434	1667	KRTDWRDRVAFRCRSIAESG*R QAIAKELELTASAEILLWDDYF APGYGVPNDEGMEAVKLLARL EGILLDPAVRLR
26193	56561	A	26340	1	1671	
26194	56562	A	26341	1067	3947	FCTVPAVYIGGPGFGARHNAS NSLKDIAELVPFAHRYGAKIFV TLNLTILHDELEPAQRLITDLYQ TGVDALIVQDMGILELDIPPIEL HASTQCDIRTEVEKAKFLSDVGF TQIVLARELNLDQIRAIHQATD ATIEFFIHGALCVAYSGQCYSH AQTGRSANRGDCSQACRLPYT LKDDQGRVVSYEKHLSSMKDN DQTANLALIDAGVRSFKIEGR YKDMSVYKNITAHYRQMLDAI IEERGDLARASSG
26195	56563	A	26342	182	881	HAEPYPYRGLLLKLGESRGCLL PASLPFSLQEFFYSGPREELAQK TLLVSVWDYDLGTADDFIGGK CDPADQDVVHTALREVTREELG LAVPEEHVWGLLRPVYDPQKA TVVPVLAVGVLDPQSLRPNSE EVDEVFALPLAHLQLQTNQGY THFCRGGHFRYTLPVFLHGPFR VWGLTAVITEFALQLAPGTQYQ PRLAGLTCGAEGLARPKQPLA SPCQASSTPGLNKGK
26196	56564	A	26343	237	338	

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26197	56565	A	26344	279	533	IHLRRILQRGQ*PRQRWRERCC ESGRGTS GPGSSQ*LTGSPQECC TPAGETG PRAHSPQ*SCWCHCC TPOGRQSICTRTSHRTA
26198	56566	A	26345	126	303	LLLSYGVGASHQSLECHHRSNH GSLWMH SKRCAGGKIRVGTPE CQ*SALERPGLPLC
26199	56567	A	26346	368	746	SLLHTTSRAPEGPSRYPGPGPPS AATKGQRTRRPLCARPP/PGLPD APL/SPAAPTTLPLPCPRVAQP AHGPPSASALSSWENRPCCRHE LAAKPPEQAARRGHARTPTAG PAPPGRRAALSGSQFP
26200	56568	A	26347	79	159	SFLGVSRRGFGFRVTGQ*WRE GQQINK
26201	56569	A	26348	1	3369	
26202	56570	A	26349	3	529	MELAKVVKSHPSAKMVLCIAT DDSHLSCLSLKFGVSLKSCR/T LLENAKKHHVEVVGVSFHIGR GCPDPQAYAQSIADARLVFEM GTELGHKMHVLDLGGGFP GTE GAKVRFEEIASVINSALDLYFPE GCGVDIFAE LGRYYVTSFTVA VSIIAKKEVLLDQPGMEEENC
26203	56571	A	26350	146	502	

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26204	56572	A	26351	3	2212	MKRSRCRDRPQPPPPDRREDGV QRAAELSQLPPRRRAPPGRQR LEERTGPAGPEGKEQPALASQ SAEIAASARLPPRLGRLLGFQK ACRCWSLNPILMALRLSLVPP DKKHPQVWRGPPLHLAPNVG LFSRVKVRSSVIEDKSMRDSR RGLSQRRRRRKKKKRGSSSKK KKRRKKKKKKKKKKRRRKN RKKKKKKRKNRKKKKRKKKEK KEEEEEERRKKEEEDDEGRGRGR RKRRKKKKKKRRSRKKKETAA AAAAAGERLGKWWPGCEPVEC VAYFLRRRLQQLRHPARQLLL QGMAGYLSSEDFVMVEEGFST RDLLKELTLGASQATTDEVAAF FVADLGAIVRKHFCLKCLPRV RPFYAVKCNSSPGVLKVLAL GLGFSCANKAEMELVQHIGIPA SKIIICANPCKQISQIKYAAKHGI QLLSFDNEMELAKVVKSHPSA NFHIGSGCPDQAYAQSIANAR LVFEMGTGLGHKMHVLDLGGG FPGTEGAKVRFEIASVINSALA DLYFPEGCGVDIFAEALGRYYV TSAFTVAVSIIAKKEVLDDQGR EEENGSTSKTIVYHLDDEGVYGF NSVLFDNICPTPLQKSSTKSLR TTIGEAFERLHRLRERQKAML EELEADTARTLTDEQKVQRYR QQLRKVQEGAQILQERLAETDR HTFLAGVASLSERLKGKIHETN
26205	56573	A	26352	1	860	MKKEDAFKAFYIVHGWNCV KGSLTRTPCCCTNCLAGGIWC MRVQIFQLENKVLPGFPWACR VDLYGQIGFDAAAQCLSLSVSK AEPLVKKAPPELREQLARKTSL SDNLKYLFDNKDIMVKQSKK KKEHSFRKNNGCIKIIAFSDHAE DFRKLGCVELGISVDSQFTHLA WINNPQREGDLGPLNIPLLAEV ASGLSEDYAVLKTDAGIAYRG RFISDGKGLV/SQITVNDLPVGR SVDEALRLVQAFQYAEHAEV CPAGWKPGTDITKLNVDGSKE

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26206	56574	A	26353	70	745	ERGSTRVIVRASSLCPRSFQSWP PVTRASESQPLTSRQQRWSDGA FKEVKLSDYKGKYVVLFFYPL DFTFVCPTETIIAFSNRAEDFRKL GCEVLGVSVDSQFTHLAWIT PRKEGLGLPLNIPLLADVT LSEYDYGVLTDGVIAYRGLFII DGKGVLRQITVNDLPVGRSV DEALRLVQAFQYTDEHGEVC PAGWKPGSDTIKPNVDDSKEL YFSKHN
26207	56575	A	26354	1	689	MAAEDELLPRLPMLLETGKQ LLDEVELAAETTGQIVQEKRA REHFINYLQCHYYHIAKFELL KTKNNSAENHTANSSMAYPSL VAMASQRQAKIERYKQKKELD HRLSAMKSAVESGQADDEHER PPVKSFILTRNTAQAKLFGASYP SLATMTVSDWYEQHRKYGALP DQGIATATPEKFRKAAQQQKY QEVKEGEDDEALYRVREWDN WKDTHPGGYGNRQNMG
26208	56576	A	26355	1	810	NYLTQCHCYHVAEFELPKTMN NSAENHTANSSMAYPSLVAMA SQRQAKIQRYKQKKELEHRLSA MKSAVESGQADDERVREYYLL HLQRWIDISLEEIESIDQEKILR ERDSSREASTSNSRQERPPVKP FILTRNMAQAKVFGAGYPSLPT MTVSDWYEQHRKYGALPDQGI AKAASSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSS KAAQQQEEQEEKEEEDDEQTL HRAREWDDWKDTHPRGYGNR QNMG
26209	56577	A	26356	223	359	RKQQDEPCGHLQSPGKPFLLS CRDPWGGLPV*LEKDRHKKS
26210	56578	A	26357	1	3855	
26211	56579	A	26358	1005	1293	SDRRYEWDCPR*LNGALLCLL LLEHPEGCPWHSVWSTGHSLEP MHFRFPSSQDLQLLLPLPGKLG YRARIRNHGHSCLQRRKTVYQ GDGPLREP
26212	56580	A	26359	763	978	

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26213	56581	A	26360	1	1217	MQRRLKRRNAGLPCCCEVPGYY REDASSPLLPKYKTNFSQCLVH FFDELRRHHLVKTRHVLFIPLNH DIMQAFTHARVIVGVKVPGIFS RHPHAVLHLGHSQIGLLMEYPD ELLWECKEDALALIRRDAPMLT DFTHINLLNAPLLDKQAEWCEV FDRGRTTSLLLFEHVHAESRDR GQAMVDLLAEYEKVLGLDCR ELPDYLLPLYEYLSVLPDDQAK EGLLNVAIPILALLGGRLKQREA PWDALLDALVQLGGSSLSND VKKQVNSEERDDTRQALDAV WEEEQVKFIEDNATACDSSPLN QYQRRFSQDVAPQYVDISAGE GQSSQLVSYWEKDVQTCLEFL PSGGFVVSASGVKLQTFETD NLVKDITFFGKISTRSLKTYLKD VTEKREQSCVNLELK
26214	56582	A	26361	1	783	
26215	56583	A	26362	2	1646	PGSTISFRRVTQREKKQPEALC QGSTSNLQFIIHPLLSAQTVEL GLSKFVPKMKMITQTS/ICYMTS LGILFLINILPGTTGQGESRRQEP GDFVKQDIGGLSPKHADPIDDD STDNITIFTRILDRLLDGYDNRL RPGLGDAVTEVKTDIYVTSFGP VSDTDMEYITDVFFRQTWHD RLKFDGPMKILPLNLLASKIW TPDTFFHNGKKSVAHNMTTPN KLLRLVDNGTLLYTMRLTIHAE CPMHLEDFPMDVHACPLKFGS YAYTTAEVVYSWTLGKNKSVE VAQDGSRLNQYDLLGHVVGTE IIRSSTGEYVVMTHFHLKRRKIG YFVIQTYLPCIMTVILSQVSFWL NRESVPARTVFGVTVLTMITTL SISARNSLPKVAYATAMDWFIA VCYAFVFSALIEFATVNYFTKR SWAWEGKKVPEALEMKKKT AAPAKKTSTTFNIVGTTYPINL AKDTEFTSISKGAAPSASSTPTII ASPKATYVQDSPTEKTYNSVS KVDKISRIFPVLFAlFNLVYWA TYVNRSAIKGMIRKQ
26216	56584	A	26363	217	559	MKKALQVAMFSLFTVIGFNAQ ANEHPHETMSEAQPQINSATGV VKGIDLAEKKITIHHDPIAAVN WPENTMRFTITPQTKMSEIKTG DKVAFNFVQQGTLSELLQVIKVR KPAQ

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26217	56585	A	26364	72	157	ERRKF**SQSSQKKNKERLQNAVILEL
26218	56586	A	26365	3	620	VSGGGWEPSGTLTAFKTASAIT TEMASRSQGIQQLLQAEKRAA EKVADARKRKARLLKQAKKEA QMEVVEQYRREREHEFQSKQQA AMGFGGNLYAEVEQATRRQV QGMQSSQQRNRERVLAAQLLGM VCDVRPQRPSDLQKEEMTTTFSP SLIIPARACRFLVRAQQSSGHLH YRAKDPVGTSLRHRSSRIHG GVPTKTCVAKT
26219	56587	A	26366	28	187	TGTESGQYHCKRRKMGPPIIK SLWARSDEPVFWG/LFGAGGM WSAIIAPVMIR
26220	56588	A	26367	1	870	MAVWPTGALALTSPAGDAGA CSTAGGPCQGARGRGSGPPA WGPDAVLEPLRGQRKPYVRPM TSTWWKKLPFYRFYMLREGTA VPAVWFSIELIFGLFALKNGPEA WAGFVDFLQNPVIVINLITLAA ALLHTKTWFELAPKAANIIVKD EKMGPPIIKSLWAEPMINPNP KRSDPEPVFWGLFGAGGMWSAI IAPVMILLVGILLPLGLFPGDAL SYERVLAFAQSFI/GRVFLFLMI VLPLWCGLHRMHAMHDLKI HVPAGKWVVFYGLAAILTVVTL IGVCTI
26221	56589	A	26368	741	894	
26222	56590	A	26369	504	558	
26223	56591	A	26370	897	1097	RKWSQSTRLPWETGPSSETSPS GPVSPTRSHLASPRRPPPTPP*S SPRRLLGAIPFGVGPLNE
26224	56592	A	26371	200	657	GPRRLSFVTGHKAYRGLGIVSG PTVPLVCAVCCSYWDPGVPRV VRLVVRLWPLCRCGGRSGDAS VAAAPLVCGGGI*DWDHCPFV CGPSLICALRPSGCGSGMACRV VLLLRCLAMFAFTSFVTEV GKFSFPPLPEFFSGFALDLSLP
26225	56593	A	26372	196	404	
26226	56594	A	26373	1	3162	
26227	56595	C	26374	287	349	
26228	56596	B	26375	366	1637	
26229	56597	A	26376	365	604	VLAVSYPCLLLL*KPIGPEDAI YALSSDFTCGSPTAAGRKQIRG EVCPRERCSVETCLSPNFHSLVS SFPFSLQGGK

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26230	56598	A	26377	1	1404	TLVRCFPPLKLIFSIFKKKAASL GSSQSSRTYAGGTASATKVSAS SGATSKSSMNPTETKAIPVSQ QMEGPHLPNKKKKHKQAVKTE PEKKSQSTKLSVVHEKKSQEGK PKEHTEPKSLPKQASDTGSNDA HNKKAVRSAAEQQPSEKSTEPK TKPQDMISAGGESVAGITAISG KPGDKKKKKSLTPAVPVESKP DKPSGKSGMDAALDDLITLG GPEETEEENTTYTGPEVSDPMS STYIEELGKREVTIPPKYRELLA KKEGITGPPADSSKPIGPDDAID ALSDFTCGSPTAAGKKTEKEE STEVLKAQSAGTVRSAAPPQEK KRKVEKDTMSDQALEALSASL GTRQAEPELDLRSIKEVDEAKA KEEKLEKCGEDDETIPSEYRLK PATDKDGKPLLPEPEEKPKPRS ESELIDELSEDFDRSECKEPPSK PTEKTEESKAAAPGSCVGGCVS
26231	56599	A	26378	1	688	ITAISGKPGDKKKKKSLTPAVP \VES\KPDKPSGKSGMDA\ALDD LIDTLGGPEETEEENTTYTGPEV SD\PMSSTYIEELGKREVTIPPK YRELLAKPIGPDDAIDALSDF TCGSPTAAGKKTEKEESTEVLK AQSAGTVRSAAPPQEKKRKVE KDTMSDQALEALSASLGTRQA EPELDLRSIKEVDEGSLPDFQQQ SLSLGLPWPKMGQFLSSTFLEG SPATQRK
26232	56600	A	26379	199	384	VYKECR*GFSHESPSPKPS/HIE *KFCMCGENGQGLRKKSSKN SFFGTSFTWVGRENVKHI

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26233	56601	A	26380	166	2172	TYILRNLYKEVMLENYRNLSL GKAVFFPFLH*FSRDLIT*YVP QSQQFLSQHVLQIFLGLCAENH FHPGNSSPGHWWKQQGQQYSHV SCWFENAEGQERGGGSKPWSA RTEERETSRAPFPLQRQSASPR KGNMNVVETEPSSAQRPNPVL DKGLKELETLRFGAINCREYEP DHNLESNFITNPRITLLGKKPYIC SDCGRSFKDRSTLIRHHRHSME KPYVCSECGRGSQKSNLSRHQ RTHSEKPYLCRECGQSFRSKSI LNRHQWTHSEEEKPYVCSEGR GFSEKSSFIHQRTTHSGEKPYVC LECGRSFCDKSTLRKHQRIHSG EKPYVCRECGRGSQNSDLIKH QRTHLDEKPYVCRECGRGFCD KSTLIHERTHSGEKPYVCGECE RGFSRKSLLL VHQRTHSGEKHY VCRECRRGFSQKSNLIRHQRTH SNEKPYICRECGRGFCDKSTLIV HERTHSGEKPYVCSECGRGFSR KSLLL VHQRTHSGEKPMQTFSG VTPQLLERTVLLAEMHSRDAL RSGTHSQPGAACCTTGAMHLCL RGTFWQPLTQRGQLQKVIPDP EIPIELKDHVWVADTLQVSFFLCP VLPSPSESSIFLCVVCINAYAV APQSGLMREKDVHVWECGPPP FARTAPITPSTQNWRLPREKY
26234	56602	A	26381	434	946	NTFCLTAMKILCMWFSRWHSR WVGMQGPSC*PQRTLWMTLS STGRSCVPAACTPAPCGRISAA GRLRCSQLLPHAPAPAACSCCP SVHISFQPL*QLRTSLWTVQMK SQVTQTQVGSHTSQAARALQG HQQVQKPGSRIRTTGGVKPQLEG PGRWLKIRLEGHSWTCRQ
26235	56603	A	26382	3	2119	

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26236	56604	A	26383	3	2237	NRRKFSVSIGFYTVMDAQYKIH TKTAHLITKESPOEEGKEMFAT MSKLKEQLTKVRK*FNALLYES QQLLIPLEELEKQMTSFYDSL KINEIITVLERAQSSALFKQKH QVRTILFKWCNSSQKMTLCLVL GSMISMLSTAKITAGYKSEVEV SVSHHCI*NCKKTLTLEKGSQS VQKFVTLSNVLKHFQDTRLQR QIADIHVAFQVICSPC*DWKKH VETNSRLMKKFESRAELEKVL RIAQEGLEEKGDPEELLRRHTV SPPFRDQRVLNAFLKACDELTD ILPEQEQQGLQEAVRKLHKQW KVSQDRTAHYLLHLKIDVEKN RFLASVEECRTELDRETCLMPQ EGSEKIKHVRVRLPHHSPHHL EKRLQLIEELCVKLPVRDPVRD TPGTCHVTLELRAAIDSTYRK LMEDDPKWKDYTSR*PQNGLW ISTNETQLKGIGEAIDTANHGE VKRAVEVSSGSLSKRGETLSWL KSRLKVLTEVSSSENAEQKQDDE LAKLSSSFKALVTLSEVQHLL THFGDCVQYKEIVKNSLEELIS GSKEVQEQAEKILDTENLFEAQ QLLHHQVKMPLSSAKKRDVQ QQIAQAQQGEGGLPDRGHEEL RKLESTLDGLERSRERQERRIQ VGAGS*ERFETNKETVVRYLFQ TGSSHERFLFSLSLESLSSELEQT KVVYGSLESIAVQEAENLVKEAS
26237	56605	A	26384	1	390	GTSLFDEEGAKIVKDLMSKAEK NGVKITLPVDFVTADDFDENAK TGQATVASGIPAGWMGLDCG/P ESSKKYAEAVTRAKQIVWNGP VGVFEWEAFARGTKALMDEV VKATSRGCITHGRSRYTKLIPI

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26238	56606	A	26385	1125	2228	NVMSHLGRPDGVMPDPKYSLE PVAVELKSLGK*VPGSGAGRL CGGGSCQARCYAGSVILLENLR FHVEEGKGKDGASGNKVGPIVIL TLLGVRA*VCKRLWLNVNDAF GTAHRAHRYQEPCLPH*EQYS YLLE*PKYFAKALESERPFLAI LGGYEELFKIML*VLF**AIT WIGGGMAFTFLKVLNNMEVGN KCQVDVK*LSMIIAGCINEKNG VKITLPVDFVTADKFDENAKTG QATVASGIPAGWMVSHLSGLV V*VNRNSVVSFIHFVWNGPVG VFEWEAFARGTKALMDEVVK ATSRGCTIIGKRSYTKLIPI*AG RILIRGRCTGGGASLELLEGEGL LFFGLFGIRVDCAVRGG
26239	56607	A	26386	2	482	TRQAWHEGPRGVPHSASLRSR RRQSAPSLTESPTSPSCISKMA LSNKLTLDKLD/VKGRVVMR VDFNVPMKNNQITNNQRIKAA VPSIKFCLDNGAKSVVLMSHL GRPDGIVMP*QVTPLEPVA/V VELKSLLGQGMFCS*RDCVSP VEKACANPPG
26240	56608	A	26387	3	378	
26241	56609	A	26388	311	578	LGIRQTLGFLSRARCGGSRRS LEMQNNAGEFVDL*VPRKCSA SNRIIGAKDHASIQMNVAEADK VTGRFNGQFKTYAISYFLNLF HH
26242	56610	A	26389	3	333	DAWDLCRVTSCLSLSRVWV QQAQPSLEMQNDAGEFVDLYV PRKCSASNRIIGAKDHASIQMN VAEVDKVTGRFNGQFKTYAIC GAIRRMGESHDLSFLRMADG IVSK
26243	56611	A	26390	23	389	LAASFLSRARCGGSRRTQALEM QNDAGEFVDLYVPRKNSAS NRIIGAKDHASIQMNVAEVDK VTGRFNGQFKTYAICGAIRRM GESDDSLRLAKADGIVSKNFL TGEESQDVGIFCHK
26244	56612	A	26391	206	354	
26245	56613	A	26392	1227	1430	GSSSRPDQEEEDLKLLKFAFSR GPPLSLVHPPPLLSYPSARR*PQ TPRPPRPHSLHLHPSPAQP
26246	56614	C	26393	17	319	

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26247	56615	A	26394	1	645	MIHEQENIKKNTKTIKKNQTEI LELKNTVTWEKNLLEVFNNNSFR QNEESVNLQTSYLSLSRGEKR KKKCEEMIRDLGQYQPGPYMH DGYSRRESGPNVPRRAQVDGG DARKGTHRRKRVLERGLWLKR EDKKAQGYKGR*KGPRV*GTD PQEEDLQRLSAETWLV*PEPR P*KAPAKKGEKVP*GRKGKAD AGKEGNNPAENGVDKTDQAQ KAEGAGDAK
26248	56616	B	26395	1	663	VMWLRYDTLSETHMHQLLGL NLLFLLSQD*VAEFHMELEWLP ATDTQTNAIKRPVSLPEPYLME GGYNKVFLLAKGNIPAKSYTFIHI LLDTRIDEMAGCIEKAYEKILFT KATWILFLNTPKQMMDNKK* GWVLGPNNYYSFASQQKLED ITIPS
26249	56617	A	26396	265	735	
26250	56618	A	26397	215	386	QLPESAYMHQLLGLNLLFLLSQ NRVAEFHTELERLPKADIQTNV YIKHPVLSLEQLMEGSYNKVFL AKGNIPAESYTFIDILLDIRDE IAGCIEKAYEKILFTEATRILFFN TPKMTDYAKKRGWVLGPNN YYSFASQQKPEDTTIPSTELAK QVIEYARQLEMIIV
26251	56619	A	26398	3	515	
26252	56620	A	26399	423	4482	KLWVILDFICLAFL*FFSTYMY SCE*ILVKLTLYFSFHYVLLIYC ECENLTGTLDLVFI*KCKSLLIW IA*TVYKIKHMEGEVKG
26253	56621	A	26400	173	174	AVSLLKHSNNDCSS/GFPTSRT ADPTSCGSH/WPWPQSLKQ*P ELYIGPF*PRLKQLGCCRAFP
26254	56622	A	26401	135	699	RDLVPCAAPAPAMAKRGQDTV WAMASEGASPNPCQLPQGVPEP AGQCRKMWG*SPHTEPLGT A*WESLELPRDLLNGFDQND NDMDNEIQAEVVSDEELVG NQSGKTGCPVPLLQLWLKGA KIQFGPWLQVQAPILASFHKV LSLQGSAGKCGVEAPTQSPH WALPSGAVRRGPSSRPQNGRS TNCLHCEPGKAADTQCQPVKA ARREVVPCKAKGAELPKTMGT DLLHQCDLGVHRHGVKGDHFGA LRFDCPTGFTWYMGVPAPLVW PIFIWNSCIYMPMPVPIVSRR

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26255	56623	A	26402	27	264	RLVEWL*PRDLLNGFDQNADNDMDNEIQAEVVS DGD EELVGNQSKGTWCPVQLQLWLKGAKIQFGPWLQRVQAPILASFHKVLSLQ
26256	56624	A	26403	624	955	VPSLGSFHVVLVLSVHRRQELRFGNLHLDFRRCEMMPGPFGRSLQQR*SPHGEPLLGQCRREMWGQSPHTESPLGH*LMEL*HPPSPRMIDPPTACAVPLEKLQALNASH
26257	56625	A	26404	851	1387	PKIVELLKYSQDQLEKRLKKDKALMGHFQDGLSYSVFKITTDQVLMGVDPGRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFGTKYLKENFSPWQQHGGWEKILGISHEEVD*NIRFVIRNTLCLLWSCARWPSDGP TG DY NVQGRWSIDVFKTHIPTGEASGEVSFV
26258	56626	A	26405	1	229	LRLRGTHVLNASHSRWRGTPEAYEGLGIRYLGV EAHDSPAFDMSIHFQTAADFIHQNKRAISALHLCKRSGIRQA*MSIHFTQTAADFIHQNKRAISALHLCKRSGIRQA
26259	56627	A	26406	2	594	SVLGLTLPAFRFKTLRRRWVQGGKVLRLKAPFGKKPRGSLTFWRASTRV RDMANNRRELRLRGITHVLNASHSRWRGTPEAYEGLGIRYLGV EAHDSPAFDMSIHFQTAADFIHRALSQPGGKILVHCAVGVSR SATLVLA*PHAVPPPLPFVEAIKKVKDHRGIIPNRGFLRQLLGLGPQLAAGSGSMRGGGEKLR
26260	56628	A	26407	605	1231	NCSNSGVWRISHKKERSIPDSKRRSRGNTKSSSPRPTTSLLEKLLTSGSPRIWVRMS*LHDKARRASFSSSSSAIKAFSSASRSSNESVSSLSNSLEGGQSKMSISSSTGVGSR LALGLYTSSEMVKGSSFILSSSLGLSSYSRAAFTGELEIKGAEMFSSLGNGTPVLRVLTLEP SLRRRTNTLLQWFP MCNWRLLRRVWI
26261	56629	A	26408	771	1121	FSPKLLPRREGRKPC EAPARTQTPRSKSTPFSQV***SVDSDPQKKGKQDRSRGGPLQERAQRESGNLLAATVVPRAERHPAISTEGPTGPPEGSAPSATSSVAAAGPAHSHR

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26262	56630	A	26409	3777	4343	DQEEPFGNSSIIQSLFTIKLNPQ SSLQEVCSLDTHNSPVRFKNS CSAKFHFKFVWNVILLQLSSE ELILSFVIPGVGHCSWSSYCYILQ PRIFPLWSFYIVYVEDSSICVSS LFPSWR*RP*HGSIK*CLSSQMG WNFQSW/NLPR/CVVLVLSIK KGL/HIWCMPDFPAFRKESLLN FRWLGHLLA
26263	56631	A	26410	473	667	PCSDWGWRSWPWNLQLEETWAL *CCSHSHKVSQEGTWMKLETI LSKLLQGQKTKHPMFSLTGGN
26264	56632	A	26411	1416	2108	QRANIQNLQRQTNLQEKRNPI NKWVKDMNRHFSKEDIYAAN RHMKKCSSLAIREMQIKTTMR YHLTPVRMVIIRKSGNDRCW GCGEIGTLLHCWWDCKLVQPL WKTWVRFRLDLQLEIPDPATP LLGIYPKDYKSCCYKDTCTRM FIAALFTIAKTWNPTPKCPSIMI DWIKMWHIYTMYYAAIKK DEFMSFVGTWMNLETILSKLL RQKQTKHRMFSLIGGN
26265	56633	A	26412	1	278	FRCCSSYYFKYFFCFFLSLLF *IFFLFLSLLFASLLFLASPLCVC YFFFIIVVAQFLNSLFHFFSLFVL CFSGLEVSIDISSVEILSSAMSIT LMGLSKAFLIT
26266	56634	A	26413	181	742	PLLKSGCISFLLRLLVKLYRFL VRRNNSTFNQVVLKRLFMSRT NRPLLSLWMIQNIKLPDRENR KAVAVGTITDDVRVQEVPKLK VCALRMTSQARSGLGAGGKIL TFDQLAPDAPKGCGLVLLSGPR KG*EVYRHFGKAPGTPYSHTKP YIRSKGRKFERTGRGLASRGYK NYRSYPLIKDCL
26267	56635	A	26414	368	675	SLSTLLSSRDCLPATISKQLRVL ARGCVVNNCFCKHLLNTCSLA GTVPG*GASSGRQKFKLLAKFK VLARLCSSGSGRGEPPSCLFLFL GATGILRLMASSS
26268	56636	A	26415	40	355	LLGNPSPVVKGRPCRHDGSEI/A PRVYFRGCS*SSHWSVSHFLSA PSHPRMLPTSRHRPPLRPLT*ER RGKRDD*PLHHP*P/CWSTCSP STSARATPTPPSGSGW

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26269	56637	A	26416	347	725	EAKRRRLPLSTLMEKRCFQPLWT RPSRKPKRGRTWRPPALNPTRI AGPPSPPAVSPFGPIPP* KGPFGSMGFLRLCFSAVQKVL APGSPA* PCLSCGPFRATLGD ARTPEKLCWLEERS
26270	56638	A	26417	525	708	IVAELIQHHQLPCHPLSGGKIK DQQVVFLSLSP* SSHNKTLTY* APKTNQRQDYPEGCNA
26271	56639	C	26418	1	1050	
26272	56640	A	26419	934	1708	PQRGVVWVLSVILHFPWLWGSGL PNSAGD*AARYSWNQILKPD WKLSSAAGISFQRS* VNFHYGEFCPKIPSGMYESKLSIITDKTP HFLPAQKTRSTPSPATAPLPGAT SPRPPRGRRRRRRCPEQQPPPPPL QAGPTAAARHRQDPLPRFSPLC FHSHPRASGAGSRPAPARVSPW TRRAPAPVSSGRGLAPKRSLS PRPPRPGQGGGRVPARRELPLA PRGLCVRLVYSLCSLCSGLPSF SLGSLVFSSSDQ
26273	56641	A	26420	630	734	TAARSGYPGRAGTLTGLHPMQ VCCRRT*PYSRGT
26274	56642	C	26421	4	90	
26275	56643	A	26422	216	305	ICWKYFCAG*CGKYFTLGRSH SYRRSDY
26276	56644	A	26423	859	1248	CVISVFRASRKSKHNVI VVFVYCSVSVGQRPAPV/QH QVLLQTQGISGYPGRAGTLTGL HPMQVCRCTRR*PYSRGT* REPS* LREGGSAPPKSVCPVW GACIKRLSSMSFSFSPFIKHA HACCRVLS
26277	56645	A	26424	132	548	SSGSWGFSGYQRCRES/CD YPPDMEIRGRVEQRVGYTIEQI NHMRDVFGLRLRAEDVFPPI VGVAAHKGGVYKTSVSVHLAQ DLALKGLRVLVEVWDHGPTR IVGLIISLGRSHSYRRSDNQTG TTVPLVSSV
26278	56646	A	26425	382	697	YAVKQAKTTFEDMTGRASLL LHKGYLEFLFLQTAAYQSGSP APQGTWSGTGSVCHCCSLAE* T ₁ PFRTTGACCGLMARTGHARA A ₁ SICPPDAVAPLSPSNWAF
26279	56647	A	26426	167	412	SYVKYFPHQPAQKYFQQIHCAI GLHNAGYPGRAGTLTGLHPMQ VCCRRT*PYTILSLQEQTDVVSL N

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26280	56648	A	26427	3794	4021	RGLCAPLPPLTPCFSPPLRRRAA SHLAPPTPLPTPQTPTTRALPS SPGLGRGA*RTVLPSPAPPEVPLA WGCRRA
26281	56649	A	26428	65	564	PHPDSGPQ*LQ*PHPDSGPR*LQ *PHPDSGPR*LQ*LQ*PHPDSGP Q*LQ*PHPDSGPQ*LQ*PHPDSG PR*LQ*PHPDSGPR*LQ*PHPDS GPR*LQ*PHPDSGPR*LQ*LQ*P HPDSGPQ*SDSGPRGHR*LQ*L Q*PHPDSGPQ*LQ*PHPDSGPR* LQ*PHPDSGPR*LQ*PHPDSGPQ *LQ*PHPDSGPQ
26282	56650	A	26429	184	438	DPAVDLCDLSSRRLFS*RYVL VMLFSISLVSFVFSVHVICNYFP ALFFVCASFCCGAGGLVEFVL MIVGDASAALLCMRCEC
26283	56651	A	26430	524	1995	
26284	56652	A	26431	601	1058	LPSSGGRCSRSPKTR*SACLVSGS PRTPAMIRSGAGQPLARSPTPT PPFCRPLTRAPQASSMTWTGTS TTTWLTCAMRTDCTGLPSTST WCFCSTRSSWPAATSGSNSRAP ARSWTLCCLSC*SASTRPGPRGP CRRQWRRRATPSRPSAR
26285	56653	A	26432	1	371	
26286	56654	A	26433	71	335	
26287	56655	A	26434	2	416	
26288	56656	A	26435	60	370	
26289	56657	A	26436	466	1454	PCVFQIGPRRIHTVVRVGGNKK YRALRLDVGNFWSGSECE*GPL GVGGKTHLNGFKIHRARPALIF LNSAA*EIGAGKDCGLPNITRN VG*GVVEDELMPHGL*RLRVFP ISP*GPHGAEPPGVCGQHLSS LLDAKFLL*AGCTRKRTRIDVV YNASNNELVRTKLKNCIVLI DSTPYRQWYESHYALALGRKK GAKLVRVTS*GLWGGQPDSS LLVMKTLSSSATEGREMRAF*A EEGQHWGVQGSRKLPGAFLP* AHIFVSPFQTPPEEEILNKKRSK KIQKKYDERKKNAKISLLLEE FQQGKLLGEKADELEVGSRRD

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26290	56658	A	26437	2	787	SQWLKLPSPHAGISRYNWD QAP*KTGGPRESYPHKKREVM KLGRPCPN/NPKIGPPAGIQHSP VCRGGYQEIPVPLRLDRGEFLP GGSECCTS*NGSSIVVLQCHL NNGAGFVPKTPGWKEFCIVASS DQQQPYRPVVTSSHLACPLGP QRKGAQAGLLEERRDF*TKKRS \KKLRKEI*LRKKKNCQNSAVL PGREQFPARGKLSRA/SRFQGP GQLWAEQDGFCA*EGQKSLEF LSLGKSKARKGQIKSFVLSPPM
26291	56659	A	26438	62	872	ANWTEPDDTKTMWRLSVPLDR SPQTQNTCTGEPLMPTGRQELPQ RGPEPMEAPAPARQSRVPAA GPVARQPHMRPPHSGQGEKQK MPGSRWPGQGRGRWGSPLS A**TRKIFTGIPILPLLPGTGRP APEEGMQSADKNRVKRRGGTQ RNSALALEFCELLFVSSKWFCALP STLRLKALSAAVALLAGDPE FGVRNVVWVWAGGVRCRVA HRTTEAGAFFPDWFWVWFAAT KRGDGETSGCEHSEPVSGSSGG SPPRGQYLPGM
26292	56660	B	26439	1	606	
26293	56661	B	26440	48	381	
26294	56662	A	26441	16	209	
26295	56663	B	26442	466	1275	
26296	56664	A	26443	2	252	
26297	56665	A	26444	95	266	
26298	56666	A	26445	119	343	CTLRQESKLSRGDLTAPPVSSPR GHRSSKKGNT*LGSMQL*AES CRAEPPRPALLCPGRSVSACQW GPEGPF
26299	56667	A	26446	1	383	NTGLGRGKAMTPSMSCRISML LQRPGGVLVGWDPDAHPVGT *RHSVAQHN*MPW*GAEGMGQ PC*WHGMGTSDBGPLSDSERPE LS/HADSEGRVSKAKQSELAP GQKR*GQKPPKGYRFQERTQR
26300	56668	B	26447	430	540	
26301	56669	A	26448	111	591	PGAPSSHSRLLAWEPVLP VASLGLGEAEDCSFLGRKAGV GPRHPR/ARRVHSGSRETRCG *QEPRPMLREPVCSAFLRTVKK LSGRVFPLAVKQVLSAAPAVP ALLRTAPKTPWDGPESAESQPP SLGPVAVLIDISDRRKQETIKAT GGPGLRR

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26302	56670	A	26449	1041	1410	QEERGVVEE*ELEGRREEKRR GRGRRGSGLEEGRRRRRRGGG DETKDKR*RRGGHRRKEKKEE RRRRRRGGGAACKEEEDRLP TRAFSCVEQQSASKSPLVELHP GPIPGPPLAAAGAC
26303	56671	A	26450	288	424	KRPAEGAPNP*GRPGIRPQA*K RPAEGAPNPRGPRRKEGRSGAK GSLDTGDDGEAWWAGSPHPS WP
26304	56672	A	26451	111	540	LPLALSNPKQEVVSGRGGQVDS QAGLMTGTRAVCCLQLCLNAS GAGDAEAMSAGPPGPGPARAD TEQLPSPSLPQVS*HWRGSASTS ATRTWPLRRRCSSMARSTCRAS ASASAGPWPWPAPVPWRHSA EPSCSQLPGPSA
26305	56673	B	26452	57	558	
26306	56674	A	26453	804	1524	ARETSHGDFLHFPLIWLFLSKG NVPAARINIMNWNQGLISHVGE GNVNRKHDVIGNFPPWCLFN VSDLVMTIGSPRQRNHFGLVM VLGTIHTFHRHVGHCRGCPWS NQASHQKGDDEHEQNPTNNA QLLGAHVFNCPFLRPFFFS P*NKCFRGELFAPSSHSPFLA SFLGAACKLQRCWSAARMGPGR KAPARIPPAQPARVPPMPGAVI VAAPPVDAPIVRICVHVCLHH
26307	56675	A	26454	2	330	SCSRSGTALGVVPLAGPVRSA LYLPAHSAGQRHQHDAGPTRG LGA1*DLPPVVTPEQSPSPCRGQ DQVPVAAAGE/PRCAPSLGSPPG LE/PVSLSSMSSPPRPPSCPLSG
26308	56676	B	26455	1	969	
26309	56677	A	26456	43	568	RSRLVFPLYFHASQGPATASRE VPGGWA WGPVAQRINGICLLH STGPEAPSTMPPTRLCGGPCGP ALPFSSQLAARGNPRSLPAAQL RALLSKISPPVVTPEQSPSPCRG QDQADACGKQVNMCSQAWG SPPGLELCPCHQ*AGPPRPPSCP LSG*FVLRGTGAPGAAPPSTV
26310	56678	A	26457	1	456	HEDAASSFOADVSLGNDAAVP LSGRGGINTYIPLIIPGFPYPTAA TTAAAFRGALRRGRRTVYGA VRAVPPTAIPAYPGVDMQPTD MHSLLLQPPPLLQPLQPLTVT VMAGCTQPTTmplPLPLAME LALWRVYTEVATADLPTEVT

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26311	56679	A	26458	609	1031	VCKSYPGHQGSSCLPDGQIQWL LHGYYGQEFQGE TH PF ^{LDG} *RG AESL*GHNSGHDQWCLGDGCC WG ^{WLL} TYERHEQLPAE ^{EAPG} GWGKDGDSRGTESTC*EAGAG AGPAHPAPPAPAAEGEPDLFQL PGQGCSRI ^{PCG}
26312	56680	A	26459	1	393	
26313	56681	A	26460	357	843	QTEGGAQT ^{DG} QQSQ ^{TQ} SSENSE SKSTPEDNKICG*KPDHK* ^{TLF} YQEISISI*RCACFP ^{PP} SRCMQGF GFVTFEKC ^{NFM} FPNVV ^{HFF} PAL FSPCYDMH*SSLSS ^N SLKCLPSI VVT ^{VHLL} NAS* ^{NF} CHILGLPL VPGFPYPTAATTA ^{AA} FRGAHLR VFV
26314	56682	A	26461	3	1172	GRAHGEAAADGGGGMQNEPL TPGYHGF ^{PARDS} QGNQEPT ^{TT} P DAMVQ ^{PF} TTIP ^{PPPP} *NGI ^{TEY} GVPH ^{TQDY} AGQ ^{TG} EHNL ^{TLY} GSTQA ^{HGEQ} SSNSP ^{STQ} NGSL ^T QTEGGAQT ^{DG} QQSQ ^{TQ} SSENSE ESKSY ^{RN} QLHVSYY ^{FLS} GFRD P ^{DFRQ} MF ^G QFGK ^{ILD} VGI ^{FN} * RGS ^{KVN} NATARV ^{MTN} KKM ^{VT} PYANG ^{WKL} SPVVGAV ^{YG} PELY AASS ^{FQAD} VSLG ^{NDAA} VPLSG RGG ^{INTY} PI ^{LI} PGFPYPTAATTA AAFRGAHLRGRGR ^{TVY} GA ^{VRA} VPPTA ^{IPAY} PGV/DLPG ^T DFTVL TSMVDMQ ^{PTDM} HSL ^{LL} QP ^{PP} LLQPLQ ^{PLTV} VMAGCTQ ^{PT} P MPLPL ^{PLAME} LALWRV ^Y TEVA TADLP ^{TEVT} VKPLQMGQ ^{PPSS}
26315	56683	A	26462	1196	1459	KQCRRCLE ^{TEV} W ^{KL} SKLQ ^{IST} KASNRQ ^{DRST} F ^{SAP} PRKSQ ^{LM} W* ^{TSLL} SYFQ ^{KL} PQSPQ ^{SATT} ALISQ ^Q PS ^{TLN} PQ ^{PW} GPC ^{PP} GG
26316	56684	A	26463	2234	2702	MLFIAAMAPPSLSSDAAM ^{TGT} I SSCLP ^{STAC} RRAFG ^{TKS} IG* ^{GPTI} PESSRWQ ^{QKGG} VSGDGRSSCR RAVAPLE ^{PVPR} AEAA ^{AR} PRPP SHGRD ^{PPPG} DP ^{PP} LRTPASAM DKSAG ^{TSCRL} SPLKALGSARAE QTMGRPAAERSY ^{PLLR} AQYSSR
26317	56685	A	26464	70	398	MLFIAAMAPPSLSSDAAM ^{TGT} I SSCLP ^{STAC} RRAFG ^{TKS} IG* ^{GPTI} PESSRWQ ^{QKGG} VSGDGRSSCR RAVAPLE ^{PVPR} AEAA ^{AR} PRPP SHGRD ^{PPPG} DP ^{PP} LRTPAS

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26318	56686	B	26465	18	123	
26319	56687	A	26466	19	347	
26320	56688	A	26467	3	746	SRKLLSKSVP*LN*SR
26321	56689	A	26468	1705	2031	CDAPGDPQPGRLRDISWLGTTDR SASPQRLA AAAA TAGNRRCCSS GPRRRPPP*PLARPRQRQP QPVVWPPAFPARWAEHTCPLA PWQPRSPPTPSQPAAVTARAS
26322	56690	A	26469	1	420	
26323	56691	A	26470	65	330	RDCEARCARGPFWWSLSPRRK GKRQKSQLISQRLERHFLSGKN RQKRPSKMAGPDGAAPLEPGA VAAPMGPKSSRGSPGRAGKAA ETS*SPGRAGKAAETS
26324	56692	A	26471	327	981	ASYQKFFQLLPDCNLAPSPHPQ VPATPSTSWGHLSPKPPGAFRRK HSSSRCPKAGHQWGGGQRNTP TAAHFRRLSAGSLQCPQLRVS PLTTGSLPPRSREPPRTAPPSPY PNCRLPKSTRTPSVGWSGPPSC GTRLQSHQEAEPAG*GSVRRPF LGP*RMPS*ALL*KHTGGL*GPP HPPMPTMCQPKQASKLQLLNC PQPSPSQGAGATMGNVG
26325	56693	A	26472	336	923	LKNIFSLPRISINIRFATLLDTPG VENLVIACLQKHS*PYF*GS*NI CLSFQDGTLYHKMHA VCLKCL *KPSLLSLL*DIERYRSHYNIEDFI YFHHQREEGHMHFALNPFI RHYTKFFLKVYL*STQTSVLS LSDILSPKI*IAVFQFNPAHSL TSALHYLVVPRPRLLPGLDDQC PGHNTFPVVSIN
26326	56694	A	26473	97	298	DNLTLLPRLECGMIMAHCSLN LTFSSDPAAS*VAGTTGT*H HAWIFVLCNWLNRGVTVKK RS

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26327	56695	A	26474	1958	3269	KFTMSILKIHARELFDSRGNPTV EVDLFTSEGLFRAAVPSGASTGI YEVLELQDNDKTRYMGKGVSK PVEPINKTIAPVLVSKKLNVTQ EKIDKLMIEMDGTENKSKFGAN AIIIGVSLAACKASAVEKGVPLY HHIADLSGNSKVLVPVFNVIN GSSHAVTKLAMQEFMVLPGVA ANFREAMPIGAEEVYHSLKNV IK EKYGDATGVGDGGAFAFNIL ENKEGLELLKTAIGKAGYTDK VIVSMDVEASEFFRSRKYDLEF KFLDDPTRYISPDCLADLYKSF I KNYPVVSTEDPFDQDDWGA W QKFTASAGIQVVEDDLRVTNPK RTASAVNEKKCNCLLLKVNQIR SVTESLQACKLAQANGWCV M VPHHSGETENTFITDLVVL*PG QLKGTGAPC*SERLAKYNQLLRI EEELGSKAKFAGRNRFP PAK
26328	56696	A	26475	2	684	HSGSSLLHFPILLINRKGFSPTG MISLMCNRVLSTHAKLQSC TP SNLPSQLPIGLSMSTPTKYR KLS FPGKTSQNITVPDSIVSP IFKETL EFISKGGSSSTCIVSPGPA*SL SNA VSSSSMSSLSNATNPQSSSH* KSCFPWYTPSVKP*PRPSS SNST PKNIPETVLSANRGPLKR TTTPG NFSSPDLSCFTGQPPSI WRPLL KLVSQFKQAEPLLTIGNC QK
26329	56697	A	26476	1284	2339	APPSARGACAASRRAAVPALPT PPSVCSGSHMSTYWPAA PR**T PGSSTAASPSPAASRA PRAASPV LTASPPLPAAASPS PAASHAPPA SPVLTASPPLPAAASPS PAASPAP PAASPVLTASPPLPAA SPALAA SPVHTASPPVHVASPP VHTASPP VHVASPPVHTASPHV HVASPPV HTASPHVHVASPPVHT ASPPVH VASPPVHVASPPVH IASPPVHT ASPHVHVASPPVHT ASPPVHVA SPPVHTASPHVHV ASPPVHTAS PPVHTASPPVHV ASPPVHVAYP PVHVASPPVHV ASPPVHVASPP VSCSGDSTSCFFPQ PGA VFPHS LAPSLGGWSHLVAALP

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26330	56698	A	26477	131	544	TGRPLRPLKQTQEIPSGCGVMG RATPGTSRLGDSVRRVRGAIPA PRSSLGRGFTCV*LTGAQLAPS LVPAAPRLPAALMDIQEPLAS AAPAATGPAQVTAATPLTTASA TPLTTETACSLGSSAASPLAPRA HCV
26331	56699	A	26478	1440	1877	PFQNLFRQNRNERTSCLCCLCMGA TWASLRALCCSPSP*HGWIW WWSTPTPFANGSVTSCSALTRS RWRPTWSEASGLWHAPAALL WKLRLPTPCFRSPISLSDDLTS HHQQGAPTMTHTCLGVGSSWE LQAFVLSYWFSPHLC
26332	56700	A	26479	56	345	ITWHLGLMMLSRSLGL*SGISFI NFPMK*EMIPY*KLS*IQNLQFQ PKVRPKGSQFGQVKH
26333	56701	A	26480	392	634	
26334	56702	A	26481	416	601	FLITDPRIWKASSDPASAKLFTFP SGFLM*AGTWMKLETIVLSKLT QEQTCKHCFSLISGS
26335	56703	C	26482	34	279	
26336	56704	A	26483	173	307	
26337	56705	A	26484	196	527	SAVAAACSRPEEDAMELVLF LCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLF VGILLISRRCKCSFNQKPSGPR R*GSPGGRTSSPPMQKPKAE
26338	56706	A	26485	597	797	PSNELKALGYTSSAWKRFSEQ QWGLSLGSSAPSRLPW*GDW ELPGEPPGDDSHRPFPGPIRAP
26339	56707	A	26486	3	184	
26340	56708	A	26487	256	635	GCVAPQIREQHAQSTENAAKPT RRIHSRQSEKPGRWHRGWVAG GWRRSKRAPARHRPCPAVCP RDGEDCSREAAGA*GLSGSSAC PTSTGASCCFCVPGQLNSVGF AVLGSKVLWTPGESPFQ
26341	56709	A	26488	1	378	
26342	56710	A	26489	1	571	

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26343	56711	A	26490	105	849	RRQDSGQSPAWPAGALLTLT HCAVPGSWAQSVLTQAPSASG TPGQRVTISCSGSSNIGNNFPVN WYQQLPGTAPKLLIYRNNQRPS GVPDFRFGSKSGTSASLAISGLQ SEDEAQYYCAAWDDSLNGSYV FGTGKVTVLGQPKANPTVTLF PPSSEELQANKATLVCLISDFYP GAVTVAWKADGSPVKAGVET NKPSKQSNKYAASSYLSLTPE QWKSHRSYSCQVTHEGSTVEK TVAPTECS
26344	56712	A	26491	129	1191	RSRPQCLGPQGRRVTISCTGSSS DIGAGYDVHWWYQQLPGTAPKL LIFRNSNRPSGVPDFRFGSKSGT SASLGHHWGSRVEDEADYYLP VPIDSSLSGTVLQARGELRQEP TSSSARRSMKKGRDLGEAQLQ LRVEKTGLRTISSMAWSPLFLT LITHCAGSWAQSVLTQPPSVSE APRQRTVTISCSGSSNIGNNAVN WYQQLPGKAPKLLIYDDLLPS GVSDRFGSKSGTSASLAISGLQ SEDEADYYCAAWDDSLNGYVF GAGTKVTVLGQPKAAPSATLF WPSFEDASDDEAEL*CAIRDYY PKAVMVA*KTNITPLKQKGDTP SPSLLTPSSDEVKSYKNLLPGFP
26345	56713	A	26492	283	840	TLPAAGFTDVISIHKTGENFCLIC GINGRFAVHCITL EEAKEYKLCK VRKIWFHDAHTIHYLDSFVKVN DTV*TGKITDFIKFDTNLGRIG VITNRKKHRGSFDVVHVKDAN GNRFAPWLSNIFVTGKCNKPWI SLPRGKGIRLTIAFHSDKWFCSD ISVQNLCKRFSQGDGTGKINSEA RRCSNLQV
26346	56714	A	26493	1	843	MARGPKKHLKRVAAPKHWMML DKLTGVFAPRPSTGPHKWRECL PFIIFLRNRLKYALTGDEVKKIC MQRFIKIDGQVR\TDITYPAGFM DVISIDKTGENFRLI*LTPKGSAF AVHRTPEEGVQSCAK**RYI VGTKRNPFI*VTHDAR\TIR\YPR NPLIQGEMDTPFQIEFKKTWPR LT*FPSKVPNTG*PCVMVTWRC LTLGRIGVITNRERHP\GSFNV VHVKDANVNRFAITRLSNIFVI GKGN\KPWISLPRGKGIRLTIAE ERDKRLAAKQSSG

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26347	56715	A	26494	375	1327	QPYFPMETVMTLEGGQKPVME SYTLHYLPCLLCLPWRNPESSE WQRQLLDFPLASAPGSGLTQH MAAPKSGQNLEAKPKGQASLV LSSRKICGVLGACACPGGPA R*VDPAPFPPLAGEAGLEGRPRP QRCAAKWQSRDLIPGLPGSTGL PFFPY/PPCSPGALLSQSPQAAG SLLARTPHAGQCPPRLRPARIL PWPASSARRYTPQPSRKGRTQT PLFSLNLLLETTTASYSLDFLLTA PEGFSPLFTASQEHQDNQEQHD FLLQDEGLRSPVKTRARLPLGL HGDKVEKAGPWSLGARESNLC SATSQRSAVAAGVPRAQPLPPK GKGWLDPTWQGRDRTQRTLR SIHHRFYGYSGWPGPLALLQ GFVRSLELPCAGSDQNRGQRLK GNPGAFAIPKTLDFSKAGKED KGGNGVCTTPSQAFDPLPRSSQ SPLGNMAVSGSSSSGWSKSSGT QEKKSLNQKRKVDEAEKKEEK EKKKEPEPNFQLLDNPARVMP AQLKVLTMPETCRYQPFKPLSI GGIILKDTSEDEELVEPVAAH GPKIEEEEQEPEPPEFEYIDD
26348	56716	B	26495	1919	2074	
26349	56717	A	26496	179	431	PPTSILRVSTSTSTSLCTS WLCS SLSWLYSWAGPFFSGKMTASC RGSGQINREIVLMLLLRS*VFVV ISPLEGGSETSPFMDL
26350	56718	A	26497	37	199	DGLPGLALGLDAQASWSASVV TGHRRPAPPGLALGGCHGPAAP P*SGPAGSPCH
26351	56719	A	26498	3	224	TGHRRPAPPGLALGGCHGPAAP P*SGPAGSPCH*TA PRGAGTLP GSRRTGTSPWHPPLPHIPDVT GGHRH
26352	56720	A	26499	151	403	MPRHRRSASVV TGHRRPAPPGL ALGGCHGPAAP*SGPAGSPCH *TA PRGAGTLP GSRRTGTSPW PHPPGLPHIPDVTGGHRH

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26353	56721	A	26500	1	465	VSPKLLPSYASRPYLVPNALSSP SVPPALSAASSAPRPRATRRRPP RGLSASWPLRRRSRQDAGAGS RRLRERQNRGRRRSDLAPTGA GLRRDRPGRQPRPGKALAPFAV PRPRTNFRGRS*KSGSQRTTPP RREICRTHSRDRPKLVGRGT ANGARALPGRGWRPGRSRSP APSVGARSEERRPRFWRSLRRR EPAPASCLRLLLSGHEADPRG GGLRRVAGRGGAEAEASAGGT LGDERALGTR
26354	56722	A	26501	1	1344	
26355	56723	A	26502	548	689	LGKFAPGLTASKAETAELCL KYPLEICTFL*GCVVCVCVCV CVL
26356	56724	A	26503	154	476	TLA*AAAASTSCSPRPPSPAS TTTRWRAPWRTR*EPPELCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVL CMTVDL
26357	56725	A	26504	920	1420	TLA*AAAASTSCSPRPPSPAS TTTRWRAPWRTR*EPPELCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVL CMTVDL*LI PTSTPTT*PSELLAPSPNSPIDTT QMSGLTATSVPKKLAFSWQQL CYISLIQPLSL
26358	56726	A	26505	1118	1403	AGWDPFLISFGLSNAISSSSSS LSSQ*ESNASE*YSSATSGSSGIS WYPRSDVASSTIDSSSWRSMEG IG*DSGRFSKVGSSDSSSLPCHL SS
26359	56727	C	26506	29	379	
26360	56728	A	26507	3	948	GVSLCCPGWSAVVGSWLTAA TFRAQAILSSSWAYREPPVRVG RRQPPLLLTRAQGRVISSFRH LHDFVWRTAGKESTSGANETG PLPERGRRPGRGPGSRSPRSH AVQREGAAGSVPAAGRDGGRA GHDVPHEGQRAEAAAGEAGGE FPLLLSDRRGRARRSPAAGALQ SRPGRARHLLHQLII*GP*EEVS L*VQQRGAVSGVDGGSASGQL RVHAEKAHLQERNPEG*RAK DPLGTVSALSEEARFQLRWLAG VSAGHGGQRAAGRDWPCPAM NRLAMPGSVLFVFLVFGSGFH CVAQARVQWCHSSL

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26361	56729	A	26508	31	202	ILITYIKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQL
26362	56730	A	26509	471	1716	FKRGQYQGQLLRPRFHGGQILYA RRQGADAAGDSDFCTEWPAAAL DSDEKCEKHFPFIEDSDTYVHH GPSVRNPRARVVLRWLRLTLH ESAAVEGLAVFPARRHREPEY SIPSPSQAFTPAVLATRVGTQLG GHTQIQNPVTAPTILGNTPTFHL TCFRIFSLPRHLFPKDKWRTL APFLRTLVLVGTESSVHLSGIDP DLLVFEQSPTYLNTRSSNRWD RLRLKAMNLDKQTTINGMLP STEAPSSTHQDLVVNTNSTSY SKELTTDFWARFTSLNESITTKI NKVSPSTDIFISNPDKTISPFEP IDTKLSHMPVPPGLNSSKQLLN KTKGYNSRNHTSANEDSVST SKTWLVSVALCTSVIFLGCCIVI LASGCCGKQGGYKPGQRKSG SLQIKNRNHNKENS
26363	56731	A	26510	410	867	LLTLRSTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRVWTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISRVFAA GQGLLGGYSNPRYSFSF
26364	56732	A	26511	135	756	VITILTPMLADTRRIERPCKKK GTTSLGQRKWLTLQDWPSVYP VA/HPFKPSAVP/LPVPNGLSK KRACPWQ*EGNLELLK/INPFS GF*LPVGN*KSTCEALKDF/CAL SGPAALGQWTRKC*GR/PFSI* QH*LFWHQDHPVRNPRARVSS LKSASFV*I*HDHAKKTLITLV GERYCKTPDVLTIKQNRWPLRS QITIMPVYL

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26365	56733	A	26512	161	2150	YLDAEKMGQKASQQLALKDSK EVPVVCVVSSEAIIVHAAQKLKE YLGFEYPPSKLCPAANTLNEIFL IHFITFCQEKGVDEWLTITTKMT KHQAFILFGADWIWTFWGSNKQ IKQLAVQTLQMSSPPPVESKP CDLSNPESRVEESSWKKSRFDK LEEFNCNLIGEDCLGLFIIFGMPG KPKDIRGVVLDVSKSQMVRSH LPGGKAVAQFVLETEDCVFIKE LLRNCLSKKDLREGGASPGSL RLAAGPPLTLNAAACPLRLAVL AAMAAAAALPAWLSLQSRARTL RAFSTAVYSATPVPTSLRVDD LHLTEIVGMLDSVLTPESSGK YRFISGEVLCRITGCFTGVRVEA KDLFGGCCSNPNEMVTWIKVI VEKEVWLYLRYILKALPPRTEK MAVDQDWPSVYPVAAPFKPSA VPLPVRMGYPVKKGVPMKEG NLELLKIPNFLHLTPVAIKKHCE ALKDFCTEWPAAALDSECKCEK HFPIEIDSTDYVSSGSPVRNPRA RVVVLRLVKLSSNLDDHAKKK LIKLVGERYKCTDVLTIKTDR CPLRRQNYDYAVYLLTVLYHE SWEYWKWEGKK*D*SRHGKSI YGENSSSERKYPGKRFSR*KLL RKNMGN*LKKSSLGTKEIEEYK KSVVSLKNEEENENSISQYKES
26366	56734	A	26513	3	1186	PASTMSIRVTQKSYKVSTSGPW FFSSCYLSGSPSAHISSLFSFRAG SSSFQGGGLGRGYGGASGMEVIT AVMVNQSLSPFIDKVFLEQQ NKMLENKWSLLQQKMAQSN LDNMFESYINLRWQLETLGR KKLKLAEELGNMQGLVEDFKN KYEDEINKYTEMENEFVLKKD VDEAYMNKVELEYRLEGPTDEI NFLRKL YEQEIRELQSQILDMS VVLSDMNSHSLDMSIIAEVKY QYEEIANRSWAEARMYQN*Y AKLSQLEAALQRAKQDMALQL HEYQELMNFKLAQDIVITYRK LLESEGSWLESGMQSMIHMK TTSGYAGSLSSAYGGLTSPSL YSLGSSFGSGAGSSSFHTSSTR AAVVKIEAQNGKLVKSSDV
26367	56735	B	26514	361	1215	

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26368	56736	A	26515	230	561	VRTRHLFCFAAAEETPVFTMA NEKPTEEVEKTENNNHINLKVAG QDGSVVQFKIKRQPTLSKLMK AYCEPRGLSVKQIRFRFGQPIS GTQRNLS*KKESVDAASFIVVL
26369	56737	A	26516	1242	1415	NSPSDSSLVWAWRRPQSRWS ERGGGANNRGGGRLLGNSVFG RK*LPHRRVSRVPNTK
26370	56738	B	26517	1	585	
26371	56739	B	26518	258	1081	
26372	56740	A	26519	42	275	TFAWSEEGTSPSIQSSWDPRCP HRNTPAQTGKPKRAWPRHPV HH*EPHGDDQDDGPAVSP*SY SQYPWPEGLDV
26373	56741	A	26520	646	1905	
26374	56742	A	26521	6510	7361	
26375	56743	A	26522	1	879	DCQDKVPRRKEPSMCSGLLRV KSWVSLQTYWKPRATQGVYV LPLTEERMVVLGASRVGKSSIV SRFLNGRFEDQYPTTIEDFHRK VYNIRGDMYQLDILDTSGNHPP PAMRRLSILTGEAHWCLGWGG RARAWRVSLGT*QILEVKSCL KNKTKEAAELPMVICGNKNDH GELCRQVPTTEALLVSGDENC AYFEVSACKNTNVDEMIFYVLF SMAKLPHEMSPALHRKISVQY GDAFHPRPFCMRRVKEMDAYG MVSPFARRPSVNSDLKYIAKAV LREGQARERDKCTIQ
26376	56744	A	26523	2	478	
26377	56745	A	26524	120	1167	GHVGHMCTGQHMASAYVGRV NVLRLKEVDRACFGEKAKQ*VG S*EELWAIWGGQREVCLGIEEA GAIHSTRHCNSQNGVRVWAPYL WALEAAPV*VQDRSSPGSQACS LPSPCALTMGTGIMPLYQEA WKPRQRPGTSGGTVSSEPHC*D AGSGCWLCPGLREVAHVS AEITYTSKHSVEVQVNVMS ENILGTSGSDSDVWSSKGRGYTAAS LLRAEDAPGPGPKVLEVPV VVRCFPFYSLGGRWQSGHLT*LE TKWRNGDIVQVLPNGKSRGH VQQQVPLLTGDA*EAGALHGFV HGGKKEAPWPLHSCPLAHCCFS GRYNRPGAVAHACNPSTLGDG
26378	56746	A	26525	225	438	
26379	56747	A	26526	216	364	

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26380	56748	A	26527	2	397	SCCSDWSAMA*SQLTAISASWV QAMLLPRRPE*LGGSNPEGTG* SERRLCHY A/HSLGDRARIHLH KKGRQEGSKEMSRAQTRRVW HATMETEQKQNYGRL*CCSPST NTRRRTSMRKNKAIAIEIERYS KGI
26381	56749	A	26528	312	1061	QQTLYSFGVSFYSSYCLIFSHG CSSSSICRRARLYHWAAPFRPP GRKRRDCTGQRKTSAGEPEIPP PLHHHHHHYSHHHHRHHHH HHHHGLQRSSKNFLLWPE*ILF CGSRRLGRAALFLLRSFSHPAK QGAESLLGKQS*KHLASTQCQGP RGRGS*EKWPRAQLGRKQPSSES AAGAAGLAHGPDLSVLERAG EK*SGLRGEGNRPFGSSSLGG HPLLQRSPAESSPAGTGVRTSH LEGRPASF
26382	56750	A	26529	161	453	SSSLPCSPSSCPHTSFFLDARQEP RTCRVVLKEL*QKQGLPHCR* QEREKSCSPSGSPDLGAPQPR VTPSLGLCSSWHLQASRRHCTP RCPQWKR
26383	56751	A	26530	301	630	RWKPKIRGSEGSAS*PQGR*LLP SGRRGATGSAESTLPKAESSAG DGPVPYPSQSSSLIMPRPNVA ATSSTKLEDLSYLDGQRNAPLR TSIRLPWHNTAGGRAQEVKA
26384	56752	A	26531	1	1394	
26385	56753	A	26532	240	1150	LLLHVPSPSPASTGPPSCGPCWP PRSPAAGRGSSSGCLAGEDPA TTHKSAGTGECGRGPVGHCGQ AHTGPSYPSGPPASCSPAASAV TRGQSCRSLTFRPGRHQIPGAE* QLPRGQGETGRTGLGHYLLLS CSSRWPLPKSGDGSPPSRWEYRD S*ERPGRRTPAPRCCSRSTGLGD GLKKFPSSY*GP*KCAPSGCGG QAPWSAGGSTCPDART*MPR ARARSWAHTGRPCFPRLLSIQA TP*RTGGRTCGFCLAS**GSRRG RPSSAESLPAPPGCGQH**PER SARLSWGGGMRGPR
26386	56754	A	26533	1463	1627	

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26387	56755	A	26534	1	1758	MHKYVRYSTVHNSEDMESTQ MSINDRLDKENIIHHRGILCSH KKKQDQHVLCNKIGEAGNHYPQ QRNTGTEKIQCVLTYKWKLN NKNTWTQSEEQYAVGPVGGRI GRLTNNRHTQDSSEWVRGVTA FWSRGANNALDIPAFHKFSEGR GSLHTHDGPPGPTSSLKLSFSHS FDSTGLCRPHDLVGLIIPMTVN ITSQLDWLEDAQMAGEALFLE GKLTTRKDIYTENPSLHHHHQR PKVDKTTKMGKKQNRKTGNS KTQASAPPPKERSSSPATEQSW MENDFDELREEGFRSSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERVSAAMED EMNEMKREGKFRDKRIKRENEQ SLQEIWDYVYKRPNLRLIGVPES DVENGTKLENTLQDIQENFPN LARQANVQIQEIQTTPQRYSSR RATPRHIIVRFTKVMKEKMLR AAREKGRVTLKKGPIRLTADLS AETLQARR/DVGANIQHS*RKE FSTQNFISSQTKLHK*RRNKILY RQANAERFCHHQACPKRAPEG SAKHGKEQVPVAAAKSCQNV
26388	56756	A	26535	620	886	INGVILSKPPLPPISTPIAGALL PLTKEQRGDF*KPSRNMRTSCW KTPESRANFLKFRPRSHCLTRM GSSCLLPSTCLSSSSSTFHH
26389	56757	A	26536	237	415	RCLQRPSAGTAGHPSPAGRPPL AAGLAG*RARHRSDLPGSAASS QESWCLRAAIPAPAA
26390	56758	A	26537	373	691	
26391	56759	A	26538	2	233	
26392	56760	A	26539	5	68	ALQWEEKHEL*EQSLHRKPGG
26393	56761	A	26540	184	434	GRRRGCTVGEAAVTQSLSLCS HEGRAIRHQRDSASIVLLDQ*Y TRHPVLDKLLAWI*ALAEKAT LGSAIAAEWKITPAFSFP
26394	56762	A	26541	466	683	GRPHSLPHPHADSSSLTTDCS* WRWIFKHKTDIRHQRVHTGQ KPFKC*Q*GKAFRHSFDTVTKHQ RTDAVGLHQVTCLGGVLLWGA HWRGHPSYSLWSAHCCQHGGE GASGGGLSLHLDRISLDAAGRP QPVLPTGQNILVGPLPQISLCS RSLCVLRDLGSLSPGEEGSH SQKWTSEQVKLFRSRHQSTSDV

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26395	56763	A	26542	194	558	GCDRPSRRPGAPRPPAATASC PPRSCWPLVPSHCP*PCRKRRY PGERRTSPAPPVPPGPGRPAG*T PPCELRPSSTHVALGLALPGSE GTGLRTSVRARDRLHRRTRERA AAGTAPGP
26396	56764	A	26543	1	248	MVAIHNDADAKCWGDVEQLE LSFTAALPVLPHPSLPGERPLQE AVAFCLWLLVDVLLKATVSKV GGGSALASVARVMKAQAFSPL LRILHKASTSSFRARKDSAHTPS CLLTSPGPERAGPLTQDSCQSPS HDSFRAPALLEPSSALSTAVASL RRREERLEPEQRVGELGSLGER QHEPSDNHDFQPKSKQEQLQK TLQPSGGPHCSSLLLMVFWWK QWRKTEPLKAERTGYKEKEIST KCSSPSGQLSQSSAAGPAWPE DARPEATWSATLLSFDPCKND SIEEPCSVHISCTAYS DPLKIHNS YRECGLCEPVNLEVADPSSSR ELWFRAGAQQAGAMQGVTEL RPPEFVKSRRKPVQVSGHMGNC LSKGKRFGLHCQYKQGLPQRH QLQAEERESGMRTTGGAAYAV LTTGVSPWWIWIWERRWPCAF PGKNEEPAGKVPPFSELVLTQ RC**CQMLGGCGAIGALIHCCS ACAASPFSPWRKAPPRGCCFSL LASGRCAPEGNCLKGGRQRQT CQCQSGYESTGF
26397	56765	A	26544	423	621	LPSRGAGLGTCSPPCLSLPSPPW APVRPEPPR*SPPPAPQRPVPS TT QGLNCAGAGHTGRQLHR
26398	56766	A	26545	1162	2027	MTPEPEWSL*VGNYKRTVKRI DDGHRCLCSL MNCLHERARGV SRADPTMAGAE*PAASLPCTGP QYGTVEKAWMAFMSEAERVS ELHLEV KASLMNDDFEKIKNW QKEAFHKQMMGGFKETKEAE DGRKAQKPWAKKLE
26399	56767	A	26546	1	504	

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26400	56768	A	26547	3	1215	QTMVFLTPILVAILCILVVWIFK NADRSMEKKKGEPRTAEARP WVDEDLKSSDLHQAGAGGN AVEGVQSKVNGRATGFASKL DIGKRRREGLEGTGSYPKTHA YALKKSGPWNPGTWQHRKIVR GLQFYTVFFPHSSVLAFLAPVID PSVASSSLRSSTTDNELAESE FADADEWQESEENVHIFPSHN HYPEKEMVKRSQEFYELLNKR RSVRFISNEQVPMVIDNVIRVT GTAPSGAHTEPWTFVVVKDPD VKHKIRKIIIEEEEINYMKRMG HRWVTDLKLHRTNWIKEYLDT APILILIFKQVHGAANGKKV HYNEISVSIACGILLAVF*NAG LVTVTTPLCNCPRLRVLLGRP AHEKLLMLLPVGYPKSKEATVP DLKRKPLDQIMV
26401	56769	A	26548	3	263	RPGEMACKYPLRCSGARVERL AKKKAHAACLLWTATIKVITNSV KLRRSS*GNRLKPSILC*DMKA LRQYPMPLRAWLLPMVVWVM
26402	56770	A	26549	82	318	SGEAGKEEGTRMVRIRPEPKRS LLWTATIKVITNSVKLRRSS*GN RLKPSILC*DMKALRQYPMPLR AWLLPMVVVRVMV
26403	56771	A	26550	91	714	SESLVLVWCGRVSCVLFVCVD VCVLVGGSGVAVRCFGGRGCG PRRVGRRWSCWGWCGAVLIR RVCLAVMFGALCVHPLLYPR TLLLRGQKVDRFKTNLSSGESL VTLVIFPAHGLARSFNLNVL FGVHFIAVEFWHAGVIVNKQ VKGKILAKRINALIEHIKHSKSQ DSFLHCANEQRQT*QACAGPCM GPEPQOACLNTCIRS
26404	56772	A	26551	29	363	FAKMTNTKGKRRGTRYMFSPR FRKHGVVPLATYMRITYKKGDI VDIKGMGTVQKGMPHKCYHG KTGRVYNVTQHAVGIVVKNQV KGKILAKRINRIEHIKHSKSR DSFLKR

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26405	56773	A	26552	186	512	FHLSKHRAPPYPVTAPPRTSWG SLVKQVNESNGSRLRLTSLVHE DLEGVSVVSGMNCDSALARYII ILETLIYLIISPRCWIIDSSGACSG LAMYLLPLGGDDGVLLCTPNFM AWRSNRTQFMMRSSSHMVDAS PRGRHMSPREAFGYSSRASHM LLSLLAPPWPQLMGRGLGCQQ QERPQECVPLGMTRSPYSEIHF GSSRALGSSPGSCAHEVLGPSIL TVNPFIPGSSVHVWPSNGNETN KLPHTRAGSCGSATCSVKRWG PQKPRPLPKPPLVPQALLVRG PAAAREEA VQPPKEEVTQRP GG HSSPGVFAHLKGPRSVVEIRME YGEE*PPGRCVTSSFGGWTASS LAAAGPLTSRRAWGTSGGFGR GRGFWGPQRLTEQVAEPQDPA LVCGSLVSLVLLGQTCTEDPGI KGFTVRMLGPKTSWAQDGPED PRAREEPKWISL
26406	56774	A	26553	1	382	FRTSCRQLSAPPARSLRPPG GG/EPAPGRTSRGHRPQM*SGT PAPRPPARSTVSPASPLPKPRAG RCGSRPRSACSTFRPC*SLASVS SAKTQGWKMWQPATERLQHF QTMLKSKLNVLTLLKKEPLPAVI FHEPEAIELCTTTPMLKTRTHSG CKV
26407	56775	A	26554	797	1213	AWLKFLLGTRRFLRFKSYFSID SARSLVPGRWAPGRTSRGHRP QM*SGTPAPRPPARSTVSPASPL PKPRAGRCGSRPRSACR*GAPG SRGPAFPRRTPSVTRWALGLPW LQGLRTAFWCQILSRVTAATLP DKIH
26408	56776	A	26555	1002	1655	KEFCIYNRNPACSYGVAVGV LAFLTCLLYLALDVYFPQISSVK DRKKAVLSDIGVSGEPHPACTP CTESTEGCPGHRRRKDNPLNEG TDAARAAJAFSFFSIFTWVSTAT AHQPTLVPPH*APGWVVPFAS AQP*ASPACRGRCQPCITPGSEVA GAPSTLGGQGRHYMDPSQDSS MPYAPYVEPTGPDAGMGGT YQQPANTFDTPEQGYQSQGY

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26409	56777	A	26556	262	628	QHFQTPWPWPLCAAAGTSAGT SHSGSSSGAFSSWPCWTA AEPA ARKRGRPAGSWSSPATGAPGR CRHRILSRGAGGSA GFVCSGLR GIGPLGI*LSGTFPGLTAGPETPA TERAPGASQHFR
26410	56778	A	26557	1098	1599	RIRKSHHCINTVTLGRGNSLGLK DFVRESPPGGDRNLVQGTHKHR GLGRFAQPHGTSAGTSHCGSSS GAFSSWPCWTA AEPAARKRGR PAGSWSSPATGAPGRCRHRILS RGAGGSA GFVCSGLAESGL*ES SSPGRSQG*PQGQRHPQPNGLP APPSTSVSVLVRISR
26411	56779	A	26558	440	698	IKLWAATFIKVCRLSFSCGMSIL *RCTGSKSCCCRRPLWAGPT SCAGGCGCCWGP GPPAELGPD TPAAEEAAEACCWDAIFLA
26412	56780	A	26559	448	576	
26413	56781	A	26560	513	782	EIWWAWTKWCGCWVVSFC HLCGRHC*GTCWSSETWR*MC GTSGTAPPCECWREGKDDCGR DRPMETHGCCSSFSISSPRAGKD ATTGT
26414	56782	A	26561	798	1505	FLRATSPSGHHFSYHLWIWISLR SFLCNECSESCLLNSSMWQAP GLSHYSLLLIWLWLVFQTLNPR HLLHLLPSPLNVVDRLCSCQHH HHQ*CHHLHNLH*NHSHHRH HHHQ*RLPLHYHLHQHHHHHQ NHCQQHHHRYHQHHYQHHDH HYRHHHPWLAGARALCDSND AGCPGSGDGDWRPYSADSDSL DALSFPRPLFPDCQSLRGLASA VIQGYNWLVLTENHILHFLF

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26415	56783	A	26562	1	1073	MHATNSSSVPEIQVEALCPLL TQPKSPSITSAMLCQLKKPQPS RSKEREADPISCGPECQGNWDL CVEAATGLYGDGHLRDSRTR VLMITIGTYRDLQGLEGRAGHV AELHVLVPVWAIQDRGYVLWC WTASLHPRDVAREQGFPNDCT WALGCTLTAESTHTHSAALAR QAYSQLSKKPTLLNEPEHITEK KFINLARFEALNSRTWLGVLV WIAQIQDVPVTVESTTGQRAAR ISPREADRTL VKGVQGIQTIV MSVPGRKEGDKLKEVSDGRE ANQAGMKWGKECKSSGTEN AMSGKEVGILQEEKGDWSHGV VRGWQEKWMTYNFWACGRG KNATCRLEMTRTSENDLKHNQ EGLWHGRERAMLGDTHTLAW REEEMEQQALRIHSLYGKTSQ QRALGSWWVERFMGMRSGSS DCNGLVTEG*TLQSA CIPEPTCS H*GSPAP*LHP*GAEKQSSTTEH SPCPGLPQAERGAQPRVPPCP QDPADPCKFQWS
26416	56784	A	26563	1	387	MESTEIGHIYEQFTLT KMTKRF NKEQLVLISLALLDSGHTSNL AWPSCLVSGVSGSCRWVCGLT D/CQE*SLRPSQAGVCRRTSPD PVCLGVTRGGCRTEKIAACSFL WKLPRPGAPARCQPELSCM
26417	56785	A	26564	47	472	LLRLHFWQEERLKPSRKKITKK HTKKRTASLILHAMICCRSLNSS KTKNTKCLNSINQRLKILSLQK GDPLESTCRH*CCHVHRRTKAP GQRRVGRQHVV SAGNHRHPHK GDPLESTCRHATVTGQGLLEFA GGPLQTLFA
26418	56786	A	26565	329	615	TKTEIGTRSINELRQQLFATTNT FFFPISFGESNTTSTSLTLKNSAI WCPTGTKLPEGRGTGSNLCCSAA SAGDTQANRVWSGSPAN/C*QT CRRRSC

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26419	56787	A	26566	525	716	PTCLLTTPPSKGRQTPYATGELR LASDGCPSGTKLPEEGAGSNTQ ANRVWVSGPSANSSRPAAEGPDC CRTTCRTTCWKPTTVTCSST PCCQPACCVSSCCQPCCRPCC VTSCCQPSCCSTPCCQPTCCGSS CCGQTS CGSSCGQSSCAPVYC VSSCCQPSCC*SGPSSAGLLEFA EGPLQTLFAWVLLPAPSSGSFV PDGHPSDASRSPVA
26420	56788	A	26567	3	390	EGPCKCGWCC/RSPTML/CPT VFITCRPGDSLRLHHQGRPFQ AQN/CQPFQGTSS*LQEFFPIQ WLECRRALAGIWQVPLWDEA SLPEEGAGSNLCCSAASTGDTQ ANRVWNGPPANSSRPAGEEAD
26421	56789	A	26568	658	1005	NSKYWTPSGPPRLASGAIYGN SLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGSGPHL GPDG*MVGSVQVQHDNELYFC/ APAGSYPLWVKALPQPPSQPL KPVASM
26422	56790	A	26569	1149	1715	VLQLNLPGPVASWCSRDVGPP ARPIPPAPHTLSSAGPSAAAP GPARQLPHPRGDSRTARLLPGQ GSS*SWR*GAWQSGCQSYRKP GLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGSGPHL GPDG*MVGVPSPGAGAAPEPA PGLWDPPGHCSQASTPPGACKE RETLPTALPRLS
26423	56791	A	26570	32	335	LWSLFDHHVQRAVCDRAKYR EGRRPRAVKVYTINLESQYLLI QGVPAVGVMKELVERFALYGA IEQYNALDEYPARRLY*SLSY*I YELTKCKDSQEKNG
26424	56792	A	26571	407	842	TEPLITINRLQRRRSAPVAAAG PAGTLARRAPAVTAERAAGPG PASVHRRPGWRRASGPAAAQ ALRPPPPR*PRDSASPLSRKELL KLLGTKHYGRLTATEAQAPQG QHKLLCRETGELVPHWAGSHY RGISNPINNIDHIL
26425	56793	A	26572	409	614	GLPPPAVGDRQCLPVRH*RPS QTIRAEQEPSAAPRRKPKG CRRSRGSSPLADNLGDLGSGGQ GG

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26426	56794	A	26573	3	266	GNHCRRQYRDAQ*W*EAGRV SSCAGSARLGKAKGRGPQGV MGNE/MRSRRAQEFKKYLHKS TSR*KSHTGPEALSTSPGAKKE GCSQ
26427	56795	A	26574	36	384	GWYCSSRSVDVCSGGNSSAHSQ LPHQLPLRLRPGGSGHPRESSSP SKQRGGPVGDRQCLPVRIH*RP SQTIRAEQEPSRAAPKRRAKE GTRRSRGSSPHEKLGDLGSGG QEVVP
26428	56796	A	26575	101	334	CSTSKEK WQCGLRAECSPVFPA TEVPEYSC*GRKPSHLSCHRAP TLEEAA NRKWPCTQYDAIQNA CYNDLSLVRLS
26429	56797	A	26576	435	761	QGTNTWVPHVLRLLGLHTSP PEGIAELPRSLPSLTHQACQLD CVLVAIGTAILVAQTATTSPPIC GEADAH PASTPLPPSWPPQGRQ LSC*NPLGWPWPSGRVQTP
26430	56798	A	26577	38	236	RLLPLENCLSSASGTCAHQAP LLLCSCPNC*SCCCCHCCCP GCCCHWCHRPSTKGN SATFTA
26431	56799	A	26578	1316	1548	FFSITGLSSVAGGQFVNLYLKR LNSNFIYLSGYVIVYINIVFIYC I*KFVLHVTLRTDCCKTIVKKH VFRLFLKAM
26432	56800	A	26579	1	272	RPVNSRLDDFVAACAAMAKIK ARDLRGKKKEELLKQLDDLKV ELSQLRVAKVTGGAASKLSKM *VRRPDHSPRGWGAVHRDRR RISKLA
26433	56801	A	26580	1	363	
26434	56802	A	26581	286	867	IYALSLGAGGAAAAGLCSNEP RFKARDLRGKKKEELLKQLD/ DLKGGSCPOLTRSPKVIETRCGP PKLSKIR/VVRKSIC/RVFSPIYIP DFRKENLQNSYKG/KKYKPLG PCGP*GRTRAMRPPGSKARRE NLEGPKEAGSGKGAFTRCGK *RGSRALRGRLCQLKHKENLKT KKQQRKERLYPLRKYAVKA
26435	56803	A	26582	164	346	LHPGRRPGLTHLGVPSPGPGPT EKLAPGKPSSAACAPSPALD* HIAFGVDALCPTFGLN

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26436	56804	A	26583	316	723	LVGGWGLWGGHLGPLYGQA QGASPLPPPPPAHRPPPHRHST EHGVEHPLVT*TAPLSPCLGFR LGQALHRGASTKGLLTGGVW GLHSWPIGDGRATHEAVVRAS PWPSRLGTHGVRGGRDVQEG AELPAV
26437	56805	A	26584	177	418	RNPVVAQGLLACACRMFKVGNR TPSSSAEWPFSSAFPKKGLPKA TSEPLFPHKRR/PLASVPSHREC RPPLGASKTAPRD
26438	56806	C	26585	149	277	
26439	56807	A	26586	1037	1455	EESYGLLSVPSVTGSLLLQDLH KLGCHQFGHKKRRVSGIWMMA VLPFFFRCPHILLLENPRAN GPARQPTNHQPP*KAGTQLPNS VAPVQSGTGFPTPARKARAPT WPGAARPPGTASNKSPARSPCS SPSFSILP
26440	56808	A	26587	175	450	
26441	56809	A	26588	77	337	RDHEPTRRKKVTRHPNVRRNK LRTRRL*EL*HSLRGSAAFLKE GRPWRSGGGAQRR*KYWRKG KYSKGKMQSWSRVYCSLAKVRA
26442	56810	A	26589	1043	1555	ALRQGPAGARAPNMDSSVSR QVPGPOVCRAVPTEILASPAVE RAPAAALSSTTIWMPMSLCPW RPVLAACSTMVTRGRSTMYLP TTTGNAGCTWPKASLATRWLS SPMGRQARSLMLGAQVTLSDW RSMPWRRRRGRSSGRNLSTI*WR LDWSLRRTRWSGRAWMSGIST
26443	56811	A	26591	313	462	VCFTPEPARPRIRQTRPDRRNSE HIRT/RRRKKLRLTHLNRNKL WTRHL
26444	56812	A	26592	630	777	KERRGREKKKEEEKRRRRGRG GRRRKRRRRRGRGRGRGRGR* KERRGREKKKEEEKRRRRGRG GRRRKRRRRRGRGRGRGRGR RGSRRFL
26445	56813	A	26593	284	461	HSPGGSAAFLKSVRRRTHQFR TH*FHHKNRITFTSR*SH*RMQR WDQREVKVFL
26446	56814	A	26594	573	968	AQRFCBSQWRCSRRVLEENP APLDTTPLSGRSKSSGRGLVLS LGL**PPSTRRSSHL*QPSSP*AS TFLQVRMTAPSL*PQPPA*KL RSSPLLLTKNPFEEAAAF*SRGP PVSLKDTASLQAFLGW

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26447	56815	A	26595	3	699	RGRSRANS PQLLEGGADPTVG DIGHLSVGVGPVHNNAVGCQP DQTTPKHLADNPGPWTLDALT YQPHAANSCHKRGIAAS*SLMII MVIIIFLVLLFWENEVNDEAVMS TLEHLHVDYPQNDVPVPARYC NHMIIQRVIREPDHTCKKEHVFI HERPRKINGICISPKKVACQNLS AIFCFQSETKFKMTVCQLIEGTR YPACRYHYSPTEGFVLVTCDDL RPDSFLGYVK
26448	56816	A	26596	2	483	
26449	56817	A	26597	2	1041	WPQDGSCTWLAVAMGCWLAT QQGSLTRVPVATSGIQGCQAAP SPMWAAWTHGWASCYFRAAL QLPLPPGSTGNGSMSTSTAYSAS SSPGFM/YTKAQGERSDHKENV FYVQHQQYVGGATQAFAKEN NQKAYKETYGVSHTRHMLQ IPKQQNEKYVQPQFDQSTIKNI ESAKGLDVWDSWPLQNAAGT VAEYNGYHVVFALAGSPKDAD DTSIYMFYQKVGDNIDSWKNN AGRVFKDSDKFDANDPILKDQT QEWSGSATFTSDGKIRLFYTDY SGKHYGKQSLTTAQHLQQYLT YKRSFSIVVDAILPPLKRAAW PKSRHPPQVGLMEVQHLFPIN NFEEHV
26450	56818	A	26598	116	338	

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26451	56819	A	26599	971	2485	FISSCFVRACGTLNPGVTMFYVI LGKFCDFAEPPFPHVMQEQLR VVGKGLWGFVRVSLSGFRIHGP HOKTASLAQVHKAVLHDGRTV AVKVQHPKVRAQSSKDILLME VRALPFSFLCPQSTFMWLVEA KKNLPLELDFLNEGRNAEKVSQ MLRHFDLKVGGTMQCRVWW SGGLMEFVDGGQVNDRDYME RNKIDVNEVRSRAQGCCAGER GVNGFVHCDPHPGNVLVKHP GTGKAEIVLLDHGLYQVEEAFV TQPWGLWGQSLIWTDMKRVK EYSQRLGAGDLYPLFACMLTA RSWDSVNRGISQAPVTATEVG GPSRPCLFLNAEISHLNHNVP MLLILKNTDLLRGIEAALGTRA SASSFLNMSRCIRALAE*VWA PPSPPLLA*ISFSEAFNLWQINL HELILRVKGLKLADRVLALICW LFPAPLCTVHVITILLWNPLRT LWPLSQGGQAEALWHSSLFFSKK TQQTFFFLVCAIGLDVPTTSVK
26452	56820	A	26600	831	1205	RKEGQGPSVHPLGSGCFPPGHA FWEALEANTWVPCVRL*RTVP SAELLGLAPGGRWRVNRDRG RVAAASSLGEPYSSPADASFP RSDSGGLDRQGGSCRYPKELFG SHPQARCTEGSLQVL
26453	56821	A	26601	377	962	LFSIFITQDPKRELLDVGNIGR LEQRMITVVLKACV**LCSI*AN ASVIYIFQEWTDHLLVL*SMC HLNLSPLCSLHSIYRNREGGS WGRKKTIC*LRCFISQNDISIPQE DFTPEMQILE*NLV*KILIAWFI VFSGAKSKPYLTVDOMMDFIN LKQRDPRLNEILYPPLKQEQVQ VLIEKYEPNNLSLARK
26454	56822	A	26602	1	810	MDAKKRKLYKYASTDSPAFAI TFIIMPYMENQAAKLAERLSL NELVFSSEALTHSETFLPOPDNR HQNMSSTIHTAPIDTALGGNPA FLYLFLQDFQPTQDNLSASVTP SAGV SARLAPPTPGPFTDVVV LDVLDEVGQGGVEESAAPESA GIGEEGGGDACHGATSRA*P*Q ASPPPPSSPIPADSGAADSTSP WPTSSSTSRTTTSVNGPGVGGG ARRAETPAEGVTDASELSCVG

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26455	56823	A	26603	28	457	GGIPDSTARLSILTPRHHLQRSC SCNGTATRFSGQSYVRYRAPAA RNWHIHFYKLTLPQQAILLFTN ETASVSLKGFEGCLDAVVVNEE ALDLLAPG/NDGGRLAGDTSPLH PVLPPQ*LLQPEHMPQWWEVL MDPRGRRLCLQMS
26456	56824	B	26604	205	1722	
26457	56825	A	26605	11	374	VSPSRSGIPGTHASGQL*TGDR S/GPMGPPITATQ*DGSDSAYH GLATLHALLPALPGAAGF/PSGT SEPCPSSPC/GQHHAAGQLGHD LPVHCSEDP RPQPPPLGGPLEDL PSLLWHSDFFI
26458	56826	A	26606	69	551	QSGRSPQHVFPSVRGSGARSRG WLVHPSQYHHNPQRIYSACGR SGEHISPGYPCS/DGHDAVDQ ADGTHHDACIFH/PRGSPRSP/G QCCLLTGGSRSRGTSGASATPG GRRGGPAQGGG/PASRNSSVEE LTARVLAPAPALASAPQTLPL GFSISPSTK
26459	56827	A	26607	476	1016	CLWLLSCLYCSLGDCCLLWVAV SVLCQVSAPRQALCFAPGENGD GGQQGLRGAPP GPGRGPAPQP GPGYPGARQRGSPQP*LSSEP GPYLRLSRSGGR*GPGRCCSRSP PGR*PVQAGDEDDQDAGSHI*T QPRVSEEGTDEDQWSLPQEV SASVPYQPLSHCQTVPASLQPH CLFS
26460	56828	A	26609	247	342	RSIMPWLPKSGGWEVSSIPP*RC LHQLWSTSRNMAL/HVRVLQT EQAVKEYNALVAQGVVRVGGV FHSTC*WSLKRRIH
26461	56829	A	26610	129	272	NDTVSGLGRLESPTLMRQRNV CSHCYPGSAK*GYMIYKDALPR RTSL
26462	56830	A	26611	133	453	QVDPNTVLRNAVHTNTYLQGL THPSANHKSLYTLNNFLHICR LHTRRMHGKTGRVYGITQRAV GIVVNK*VTGQILAKRIVPIEH KHTKSQ*SFL*ELRSPVAS
26463	56831	A	26612	352	543	VPSINCGVPQGNMMLMCRVLQ TEQAVKEYNALVAQGVVRVGG VFHSTSDGSLKRRIH*VPKKK

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26464	56832	A	26613	576	927	FAERTRTHH*PKPRWKALGC RARTAVTSRGCLAPSRRRRLP GRRAASQPGPNADPKACRPWN PRGSQVHAKRNALCFRSADAP PRPDASPGQIFPGRRRKECQTC KTRVRLGCL
26465	56833	A	26614	67	415	ALARKLPTNFQWVKKIDASPGS PIPLNAP*PSPSVQTTPTTGHPG RALSTVSEVPAGARLTYRVFP TRCKRSLILPSPVWVSRIPTAK SPILISSPGGAHAASVSALTIVS GYE
26466	56834	A	26615	87	347	GIRY*LCHGFYHAYLGFRRTS SPLQVSRPPRGQTQSEP*AQSP RSPELELGLHTASHRAANAAS SFHLRFPGFGFHPRPSPLF
26467	56835	A	26616	3	175	GFVTSSFFLGCLSPFDAYDLVFL LARE*HWHK*TQSILTLIAQCVF PEQPKRLCWVS
26468	56836	A	26617	539	788	EKEVPTLLDCCALGQ*KCKMI QLLWKMV*SFSTKLNLLPNNP AVVLLGIHLKELKTYVLTETCT LMFIAGSQRNLRDYFRP
26469	56837	A	26618	843	1136	VKEQVYRRIASRSVRRCSYQS RPGLLPTAGHHPQHLYSDCHG NDIYSVYYQCEHGAHSSSETG VPRFPCPWVSETAQ*TCASHP GPSAQRSAL
26470	56838	A	26619	2073	2329	LVQTSRPPDPSWA*SATVTRPE QASWARNLSRFPLGMATVSG RGLPSGPGRAMPSPAGEPAPGA AEPAPGSAIPIHRRPLLGQ
26471	56839	A	26620	723	1023	ITLLGLSLIPLISRLPWTQSWGFL SFLSTPTSLISSTPLILNTINSML TLRFLPPGGAFF*TPCEPIPTQH PHLDVSLTGISNLRPQSCFHCL HLS
26472	56840	A	26621	99	288	CLCQNKLGEGRDDNFTSQWSS AC*TFCLLAVDSAETTAES*C CCCCCCSAAGGWRLVH
26473	56841	A	26622	130	450	RQLKLTAGCAKSPWFLWLKSY HSLYLAAACLLGLTYTRLGRSQ SSPPIHSHFPPATSL*QQLHGQ PA*WLYDGPATP/SIAPPAHLLP PPWRGGTSPWLPSPPLQE
26474	56842	C	26623	1	672	
26475	56843	A	26624	408	581	LIKDESAPRTPQTVLASAQFCLL CR*ARCCRGSCCCCCCCCCC WWWCCCCYFGND
26476	56844	C	26625	66	264	

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26477	56845	A	26626	70	551	AAEDVWVVPSELYWPGPHGHC ETPRAGVFVVTSHHEEGPGAGTA SSSSKGPSPWARWGLEVSPLRWP SGQVGGAGSAESGQPLGSGFTF KAMGNLGESEARQAQLIHDRN TASHTAAAARTQAPPTPDKVQ MTWTREKLIAEKYRSRDTLSLG FKDLFSMKP*VSPLRWPSGQVG GAGSAESGQPLGSGFTTKAMG NLGESRARQAQLIHDRNTASHT AAAARTQAPPTPDKVQMTWTR EKLIAEKYRSRDTLSGFKDLFS MKP
26478	56846	A	26627	479	961	PQSSLQGNLQMPWGSCLDSST HYRPSLVGVDFQLPSFWLVICG TCKHCHRMHLHSVALFWVPLHC GWSIPRPRCPHPHPPPLRGPSC HPPSPPWACPPRTGVQSATCPF A*RPTWSFTCDPTTKRSMRGLT HILRSGEKRPLPALCARSTSGSA TTSPGT
26479	56847	A	26628	1	223	MGAVQKAYNLQKKRRRRRRGR RGRIRGRGRGRRRRRRRRRK KKKKKKKKKKKKKKKKKKKK EEEEEEEE*EEEEEEEEEEEE EEEEEEEE*EEEEEEEEEEEE FEFRRRRRRKKKKKKKKKKK KKKKKKKKKKKKKKKKE
26480	56848	A	26629	1	341	
26481	56849	A	26630	78	354	ENDSFYNDL*ATQRRRRRRRKK KKKGEERRRKEKKGEERRRR RRRRRRRRRRRRRRRRRRGRG RGRGRGRRRRRRRRRRRRR RRRRRRRRRR
26482	56850	A	26631	1	327	
26483	56851	A	26632	41	246	
26484	56852	A	26633	1	170	RKKRKKKKKKKKKKKKKKKE KEKEKE\RRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRR RRRRRRRRRTNNETGE
26485	56853	A	26634	1	282	MCIESEREEEEEEEEEEEEEE EEEERRRGRRRRKKKKKKKK KKEEEEEERRRKKKKKKKEEE EEEEER\MRKKKKKKKKKKK KKKKRQSL
26486	56854	A	26635	1	396	
26487	56855	A	26636	1	255	MLWLPQALGTAAETLACSR RRRRQLYNCLYLRKKKKEE KEKEEEKKEKEKEKEKEKRR RRRRRRRRRRRRRRRRRRRR RRRRN

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26488	56856	A	26637	1	290	MKKKKKEGRRRRKKEEGEEEEE E/DRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRTTT TTTTTT
26489	56857	A	26638	2	423	
26490	56858	A	26639	3	167	QKKEDEEKEKEEKEEEDDEEEE /ERRRRRRRRRRRRRRRRRRRR RRRRRETQEAETI
26491	56859	A	26640	1	325	MEKNEKEQEEEEKKEKNSKKK EEEEEEGGGEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR
26492	56860	A	26641	1	618	
26493	56861	A	26642	1	291	
26494	56862	A	26643	3	155	YRHLPKKKEEKEEKEEEEE EEEEEEEE/ERRRRRRRRRRRR KYEKCKL
26495	56863	A	26644	1	1410	
26496	56864	A	26645	578	842	TQEAELAVSRDHATALQPGQQ SKTPSEEEERRKKKEEEEEER KKKKKEEG/MKKEEGRRRRRR RRRRRRRRRRRRRRRRRRRRRR KKKEEEEE
26497	56865	A	26646	215	471	
26498	56866	A	26647	432	761	
26499	56867	A	26648	1	357	
26500	56868	A	26649	2	281	
26501	56869	A	26650	533	758	EQKKKKKKEKKKKEKEKEEEE EEEE\ERRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRNTEK
26502	56870	A	26651	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEETLFSNM
26503	56871	A	26652	1	279	
26504	56872	A	26653	1	795	
26505	56873	A	26654	1	642	MKKCKTSVIGIATFYLSIPHIYT PPNQTSFMAICAIEVQLTSAE PASIGFPVQKSPGHLQLNGYK SSSKQGFPPLKQESWNSSVKI TTCNVGDKKNINDRRSANMMH VNNFPFRHISWICLDRVQSETL PQEKKEEEEEERRRRRRKKKEE ERRRRRRKKKKKEEEEEEEEE/ RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRKKERISL

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26506	56874	A	26655	1	1167	MAPRPQAARLPSCGTRSQGAARPPLGTAAAYRPLLSSRLLTGGPPASSSWLAIHFRIRVGSSGGQGNQRKLYLGIQLTRDVKDLFKENYKRLLNEIKEDTNKWKNIPCSWVGRISIVKMAILPKVQAILMLVLFLHLFCKYNIVGMENAGNGHDSLSDRHLMQASANQQATQLAISRPSNQSKAQDFLRLLRKKEQTALDTFAPLKFAQKWNEGDGIRSSVIPGIQHQSLLAVLTFNSSKTSLGDRARPVSKKKKEESRKKKKKKKKKKKKKKKKKKKKKKKKRNRKNKKKKNNKKKKKNKENKKKNKKKKEKKKERKKKKRR/MEEEEEEDEEEEAEAEKEKRERKKKKEKGRRREGKRGEGKREKGRRRGRRRKNKEERRRSR
26507	56875	A	26656	342	616	RILHKSFRKLCKGSFCSTRSPTREIRSKKKKEEEEEEEEEEE/ERRRRRRRRRRRRRRRRKKRKRKRKKKKTKTKTKKKKKKKKKKKKK
26508	56876	A	26657	1	705	

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26509	56877	A	26658	1	2267	MKVELMGFAEGLAVRVREQEE VRLNWKVELLWTLRDVVKPG ANSFRVSSGSGVEFMVYNRT RVKEPIGKARWPLDADDMVV SVGTASKELKDFKVRVSYFGEQ EDQALGRSVLYLTGVDISLEVD TGRTGKVKRSQGDKKTWVWG PEGYGAILLVNCDRDNHRSAP DLTHSWMLADLQDMSPMLL SCNGPDKLFDHKLVLNVFSD SKRVRVFCARGPEDVCEAYRH VLGQNKVSYEVPRLHGDEERFF VEGLSFPDAGFTGLISFHTLLD DSNEDFSASPFTDTVVFVAP WIMTPSTLPPLEVYVCRVRNNT CFVDAVAELARKAGCKLTICPQ AENRNRDWQDEMELGYVQAP HKTLPVVFDSPRNGELQDFPYK RILGPDGFGYVTRPRDRSVSGL DSFGNLEVSPPVVANGKEYPLG RILIGGNLPGSSGRRVTQVVRD FLHAQKVQPPVELFVDWLAVG HVDEFLSFVPAPDGKGFMRLLA SPGACFKLFQEKQKCGHGRAL LFQGVVDDQVKVTISINQVLSN KDLINYNKFVQSCIDWNREVVK RELGLAECIDIIPQLFKTERKK ATAFFPDVLNMLVLGKHLGIPK PFGPIJNGCCCLEEKVRSLLLEPL GLIHTFIDDFTPYHMLHGAEYS LECRQHWGKNLYFRVGLKKK KKKKKKKEEGQEEEEEEEEEE
26510	56878	A	26659	1	990	
26511	56879	A	26660	1	235	MTAKCVCGWGVGEREREKER EEEEEEEEEEEE/ERRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR
26512	56880	A	26661	1	1101	
26513	56881	A	26662	348	806	
26514	56882	A	26663	39	684	LRCENPISSHVGHVGVSLAHT GLFSRLILADREDISENWCSLVC CVCVCVCVCVWWLCISLPGD MMTLLMKKDTLTFEETQFYIS ETVLAIDSIHQLGFHHRDIKPDN LLLSKGGHVKLSDFGCTGLKK AHRTEFYRNLNHSLSDFTFQ MNSKRKAETWKRNRRLAFST VGTPDYIAPEVFMQTGYNKL DWWSLGVIMYEMLIGKLHG

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26515	56883	A	26664	3	276	IKSIDDTSNFDEFPESDILKPTVLSSA*AVHWRQSESTLTSISFPVATSNHPETDYKNKDWFVINYTYKRFEGLTARGAIPSYMKAAK
26516	56884	A	26665	95	405	
26517	56885	A	26666	3	349	GPGGWLSLSPLVL*ALES*KEEE EEEEEEEEEEEEEEEEEEEE/ ERRRRRRRRRRRRRRRRRRRR KREKKKSVDCTEEVAKYVGL ASLRJSRVPPDTSTKEKTIEKVN RRK
26518	56886	A	26667	1	370	MHVAVWSCPTAQSSQATVDSGK TLAETESPIGLSSKVGKNIRAG EWDELKYDRFPGQKPKKKRRK RKEEEEEEEEEEEEEKKKKKK KKKKKKKKRRRRRRRRRRMQ QSHPNPTSAILAPWA
26519	56887	A	26668	1	430	MTFFPFDKRETDILLILNFSMEH CTRGGQDPLGYQTTKKGFKDTE TPEKESLESKAELGRRRKKKN KEEKEEKEKEKEKEKEKEKEK KRKKRRKKKKKKKKKKKKKK KKKKKKKKEEEEEEEGMRKR RRRRRRRRRRRRRR*RRRRRR RRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRR RRRRMRKRRRRRRRRRRRR
26520	56888	A	26669	1	708	
26521	56889	A	26670	1	1233	
26522	56890	A	26671	1	366	MSYVAVMFFCSVLGKFQMNLE EEVEKRRRRKKDKKKEKEEE EEK/DERRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRR EEEEEEEEKKKRRRTLYCM*IA CKLKYLWTVSGHILCPNTN
26523	56891	A	26672	1	667	MSKEGNNRHWDRLGEGGWRR VRVEKRLFRDYPSSHPRGAFAF TSPDSIGRCTLRFPGQMGLHQ PALIAILRSGADLSHLEGPMLA GASACAPAVSPGDQALQQHPG EGRKVPGRRRRRKEEEEEEE KRKKKKKKEEEEEEEEEEEE KKKRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRNQTKGP PCKNMLVFCPQNKAPSPCIQI AAEFSAWAR
26524	56892	A	26673	365	670	
26525	56893	A	26674	29	370	

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26526	56894	A	26675	1	1364	MEMIWPSKGMPTSTSYSNKES SLLSVVQTSYSYHTRGSSEE VESLNRPTGSEIVAINSLPTKK SPGPDGFTAIFYQRYKEELRIK YLGQLTRDVKDLFENYKPPPL NEIKEDTKKWKNI PCSWVGRIN IVKMAILPKIIVEDALQIYYDMV LVCVGVGVGSCRIVISSLEVLES RGQRIFFLVQAEQVLWAFKEVS SNCNDKSTLRGSVVKLQCTSGT SAFDIFQVGSRLVGEHRLPSVH SATYMSLT YFELAGLLEKSSQL VGSTGVEDIVAIMPEPKGKEIV SLLERNITVTMYITIGTRNLQKY ERWKKKRTKGLEYQEFGDDV KFRSLDIEAEMPDHLRLPRNM HASSPSKRTARGRNKNKSSRLT MFGVEIQEEEEEEEEEEKKKR RKEEEEEEEEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRGGRRRRRKH
26527	56895	B	26676	1	499	
26528	56896	A	26677	1	1684	
26529	56897	A	26678	2	297	
26530	56898	A	26679	68	319	IQHITS*TKKKRKRKKEEEEEEE EEERRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRSHTSIPKESTLLQSQSVGLG
26531	56899	A	26680	1	1617	
26532	56900	A	26681	92	338	LEKEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEN*VERY KKEGQW*KQRRQEKGLLPDG
26533	56901	A	26682	1	548	MVDQRHLVLTSTKKNQNNNF QVFVIENVGREPQDKIASPGA GQSCASVTADLLSRDLHFTKV PSWSSDGPYPYPACHLMSEPY FWGSCCYDTPIKTKTNEEEEG EGEEEEEEEEEEDEEEEEKEE EEEEEEEGEGEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RKPRGGR
26534	56902	A	26683	1	1215	
26535	56903	A	26684	1	571	
26536	56904	A	26685	1022	1365	TSLLPSSSIPSRLPVSVLSVRILS LWILACLAPWRWDLIRKASCL PAFSLLLSGANGSFSGLGFALL GRKEEEKEEEE*EKEKEKEKKK KKKKKKKKKKKKKKKKKKKKK KKKKKKKNF
26537	56905	A	26686	24	355	

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26538	56906	A	26687	120	594	
26539	56907	A	26688	117	487	
26540	56908	A	26689	2	2482	
26541	56909	A	26690	2	654	KGDVGEWLSAGKGESSAMFAS EQEISKDEQGTPLVGSFYWEVD SPRKESQA WAPGQEWIKLERD TTECKMFEQLKPIEPVQKTLPW VGEVAATLQEA MKRDCWREA RVKKKPVTFEDVA VNFQEEW DCLDASQRLVYQDVMSETFKN LTSVAWVRKKEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEERKKRKRREK KKKKKKKERTTTLWGNPLT
26542	56910	A	26691	789	1072	
26543	56911	A	26692	1246	2367	
26544	56912	A	26693	579	1214	
26545	56913	A	26694	119	1870	SCSRNRLPPVSESLTRPLSLA RWLPPGLRQPSSRDYWPKGRL RLSAVPSASPWALVSCLLPPSS SQEKAGKILKKRVEKQQPEEKV GKGLEESLCPSSMSNHTKERV TMTKVTLNFYSLIAQHEERE MR*RILFEKIEEGLKDDEEVING NVFLRKETEFRLRKTRLGLED FESLKVIGRGAFGEVKITATCQ VGHVYAMKILRKADMLEKEQ VKHSCSSAFILVEADSLWVVK MFYSFQDKNLNLYIMEFLPGGN YLTMKGHKDTLTEETQFYIAE TVLAIDSIHQGLFIHRDIKPDNL LLDSKVLGHWHELFPQEPRLR GFLSQCCDTPFRALRFLASPSFQ VPLHSRPDLCTGLKKAHRTEF YRNLNHSLSDFS KW*QLR*PK AETWKRNRRLVSNICGF*KN AENVSLGQVRWLTVPVPIAPE VFMQTGYNKLCDWWSLGVIM YEMLGKLGHRGLPQETYKK VMNWKETLTFPEVPISSEKAD LILRY*RTSLHLQIKSIDTSNFD EFPESDILKPTGNITTSIVSCDYK NKDWVFINYTYKRFEGLTARG
26546	56914	A	26695	271	446	YLVHILDALPRDPTALRRRQRC LGS*RKHQTRLRSGRPSSGPGG TDSVTA VSAQAOK
26547	56915	A	26696	1	171	WGVIWRENGRCFSGLLRAGLG AAWEPRVGEIKILVS*LGTC*IK LICQSWVGANPRA

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26548	56916	A	26697	1	179	MWKGPKGLDMYKGSSVSPKTS DILGRD/NSPAGLEGANSGVAN CLWRGPCGRKLWEASRN
26549	56917	A	26698	2	140	DN*KGVHKRILSKLAPELGSFK GFRSLAVNTHNSYGGKGNRPL KIR
26550	56918	A	26699	3	601	
26551	56919	A	26700	232	1809	
26552	56920	A	26701	1	851	MQQEDPEESTKSPNPTNNKKQE KKLSLFGGLFTWTRVKFGAVT QIGGPPLGDQSPVLLLQRLFSK GYRVSPSKAQISSPSVTYLSNVS LIKTLTKTLLPKEAGVIHCKG HQKASDPALGNTSADKGLFRP PPFSPHQARGFAPAQDWQIDFT QH/RP/GVRKQKYLLV*VDTFT G*VKAFPTRSEKATAVISSLLSD IIPRFGLPTSIQNSRLAFISQISQ AFFQALSIQ*NLIPYSPQSSGK VEQTNGLLKTHLTKLSLQLKK DWTVLLPALLRIRACP
26553	56921	A	26702	434	867	RLILPNRLGSPLLVWVDTFTG* VEVFPTGSEKVTAVISSLLSDIIL RFGLPTSI*SDSRPATKSSFSLSIP TLGSHDAPNPTRSSPEKHRPLSL HTIPQNFRCPTDPLFRFIFFAFF SNTLHIMGMAAEGPKSTLYC QFTEK
26554	56922	A	26703	96	415	
26555	56923	B	26704	1	933	
26556	56924	A	26705	1422	1774	DCPPSPIAFPQCTHQHHHHQYH YHHRHHRRHHHYQR*K*NPLG PLFVYCYFQNH*ACHCSWGSN EHMTIASQSAVLPQPQDSQG FFEDLELHYFFGDPSETRPGKQP KVSVQQIL
26557	56925	A	26706	355	1014	RHLRPOERAPAPSGSVSPRPGCS QAPGGLLRVGRGGMLLPGCAA VADLQEEVPFSGSWDAWAVKG EQRQGGGGVVKH*DAIPQQRV SDPGPPEPLASAPGQLSPSTPEY RRPPEGESRRHRRPDLAQDQRGA AVLLLAGARGLSPLPRIPALGA ASFPPTLQFFLQLPSSGASTTSA GFFLLVLHQPLWLLLLDFLFDN LLLLRHSLFIPHGFLKCVSIPAF
26558	56926	A	26708	95	298	GSTQVLWAAWGGAGWTPRWLP VFATWPWWQDMWPQQA WPLP QGVDIP*ACPPPLRT*WL*ENR KAGS
26559	56927	A	26709	110	195	

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26560	56928	A	26710	241	957	KSPQIGLQSGWGA VGVGM RDP KERATEASKPDLLAQRQGE GHI FILFFSDYIPIFSSYLSLQRSSRGP SFFGPFSSPHNIPCEGRONSETPP WPSLGKRSKKSSLYPLPKAPQP KSRAPSPISNNLKNFPQPSSEKDD GPQPLWPQKWPLA PLFSRSPS* DDSGPCTEYCRARRRFSFEDM AHIGPPKKVLYKIALGKFWELA DAKKRRKKGTS ETETCLLSRAT ELLPGKGRHCRGIL
26561	56929	A	26711	496	708	GMLFRGSGACRRGRTGGSGH A*PEPPVLPLLLHAPEPLNSMPH GLPAPPASPCHFPNLDSCVHSHS DTPLSVLPLPHLKSPLSSDFCS YEVKKDAILSPMLSWWAGHRS AAGED
26562	56930	A	26712	302	561	TFLLQLAAVWSADRVREALRP ALWDWRSVAVPHSPSQPQTG*R GVGVHPAAASRGGESSHPTAF DRSPPPPKPLRI*PEPSARSGLP
26563	56931	A	26713	1	411	LLVFQVHQCLHCKLL*PSYVPL GYTEAFLATQNGRVS L WAKH GHPDPFLARADFRAQESPSPN DPSWLL*YFER*WSQATTKG*N RCC*RC* LQAPSRRPEAVHTN DPR*REVREEHMLVQLVTR
26564	56932	C	26714	361	642	
26565	56933	A	26715	1805	2260	
26566	56934	A	26716	472	1667	AIHLLSLQTEFLVAERSSAAGRT TPATRAAFLAASCGPLHSCPTL LCSQLCCFSRSRVS GPKASLG IKEIASVDRVNTRRPACSTSSWL HNSGFTLSLANRDGGKRIRSET AKKGMSGDRSMKSWEVRRGY RWSSRAVRRPRACSSDGGTHF ALPMAARGSSGPSGSPANSVR QSLKSESSISAIWVAEQAGNV PRTSAQFGTGSESANTAARLIE KLLRAELDKPEIRDERIVGWWT TFGRPQLGSRVGFACCSLAARM SSTSQNLEA AFGGKFCFLWALL LGLDDTFESRISDTGSAGMLV EFFAPW*VHSESANTAARLIEK LLTAELDKPEIRDERIVGWWT FGRPQLGSRVGFACCSLAARMS STSQNLEA AFGGKFCFLWALL GL

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26567	56935	A	26717	2	237	SVRQTTATSPAHHKNSKRLIRSC QGF/HPEPPPTGACYKCPQPRIP HEPCPI/SQDPTENWTVQLTW QPLPELELWPKAV
26568	56936	A	26718	1	313	MESAQKEAVEIFGQPHAASSSG DVKPLLFIDFYKCSGEKVVCME HALRACYMCCKSGHWAKECP QPGIPKLCPI/GDPTGNQTVQ LTWQPLPELELWPKAL
26569	56937	A	26719	377	583	
26570	56938	A	26720	1221	1394	VASFYSLQQPPYPSTSFQSWR HTSISPF*FQLSFSFGIFWQPL EPLLELWPKAL
26571	56939	A	26721	160	234	
26572	56940	A	26722	163	414	
26573	56941	A	26723	212	399	YSLKDCWPLSLSLNHLILAS PFNLISLILISVPLFW*RTETRFI WQPLSEPLELWPKAL
26574	56942	A	26724	809	874	
26575	56943	A	26725	49	220	
26576	56944	A	26726	71	375	LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQT/TSRNISPI/NPEL ATSARNLATRPRNACSPGFLS RVPSVRDPTGNRTFQLTWQPL PELELWPKAL
26577	56945	A	26727	1	1011	CSEYEDSSAPVPATDLSSLSS SVPQPDGTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAH EHAGLGVQGGNGALAFNSNGH RHA/VPTISSGTGRRRTPSSAFA LLNLHQWVWFGQAFSDRLKA ALSASALLRFGSDWLPSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTRL QKRKKGMPHPAYEDLNIAIT LPANVVLHQPSGFRSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYLLHEKDPPTT SGPQT/TSRNISPI/NPRQRQV LSMDPKLRHRSRTGKAAPWC LIAGTPL
26578	56946	A	26728	150	211	
26579	56947	A	26729	445	549	
26580	56948	A	26730	193	249	
26581	56949	A	26731	372	564	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT/TSRNISPI/NPEK KETRFIRGPKTPAPVMD
26582	56950	C	26732	185	640	
26583	56951	A	26733	1662	1774	
26584	56952	A	26734	233	527	

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26585	56953	A	26735	380	731	LGSGDLPEINPLSSCSLLCEKH PPTTSGPQVTSRPNISPILNQEL ATSTRNLATRPACSPGFLLS CVPSVRDPTGNQTVQLTWQPL PEPLELWPKALCLTDSFPDLGL LTAED
26586	56954	A	26736	2	182	
26587	56955	A	26737	2	89	
26588	56956	A	26738	2	89	
26589	56957	A	26739	161	460	KMKFEFMKSSRTKDRQQEQV LEPLFTIAKTWNQPKCPSTID*1 KKMWIYITMEYYAAIKRNKIV FFAGTWMQLEAIIILSKLIQEQKT KIHMFSLIRGR
26590	56958	A	26740	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDFVPHFIRKN*SLF TIKAWNHKPKCTSVTDWIKKM WYIYITMEYYAVTRRNKIVSFA ET*MELEVIIIVSKLTQEQKTKHC MFSLTSGS
26591	56959	A	26741	902	1065	
26592	56960	A	26742	326	484	WYSWDCQLVTPWRPRIIPGLG TWMELEAIIILSKLTQEQKTKHH MFSL*SGS
26593	56961	A	26743	527	825	QPLWGLQH*EVPSCWRFS*IC YSSGLTVMLSSWLDLIRPPWTL R*PREWRQCMGENHIGRGLGF* RPWTWMELEAIIILSKPTREQKT KHYMFSLISGS
26594	56962	A	26744	398	557	HYWLGTVVHTCNPSTLGS*GR QIT*AQELETSLGNKNVGCSELI LLSTLGNRV
26595	56963	A	26745	3	359	HRPGIPIGTTISSWMDAWGRLEA RYMSYLHSRRGDHA*DKLQRD NRFASQTHSIHWAKSSCHCRFES RPFFLPSPSWSYNRSWGGESAE RTWMKQKRGTCLSHSPDLHLHP GLCQHKVGAR
26596	56964	C	26746	127	216	
26597	56965	A	26747	135	197	
26598	56966	A	26748	84	202	VLIIHRRDIMIPETVD*WEY**P* RLVPGQVQVWVKAIP
26599	56967	A	26749	483	669	
26600	56968	A	26750	1	274	EIRNKIHVSENSQIKTVKEKPSIS SSVRLKGVNKNVRASFPEDRKD YTGSKAPKGS*GYTIN*LK*NN KRKKKQNKKLMPKTEQGQKN SIR

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26601	56969	A	26751	63	398	TPLRQPCSI RN VQ QEPVGRFSGI GLPLSVARSSPWEAWPQCKWR FQ NAGD*DIRQPD RGQGRPAE PEKREP YLR SQQGA FLGSHSSGI QSQLLGLGESCSYGATGKPVHP
26602	56970	A	26752	3	231	SVHEEEKMALPLGQSHCGLLY LYY**RCFKCSFYCILFIKNAFI Y*N I*YINTHTHTHTHTHTIYIYI YNCLYI
26603	56971	A	26753	4266	4944	TDEIGASRLSRVESLAPEVKQN TTASGCELMHTEMQALRADW KWEDSVFQTQSCLENLVSQM ALSEQEFGSQVAQLEQALEQFS ALLKTTWAQQLTLLEGKNTDDEI VECW HKGQVSWLPV*KAEPR EDLKSQNLNLCRFSRDLSTYSG KVSGLIKEYNW*A*TLKGCQN KEQILQQRFRKAFRDFQWL NAKITTA KCFDIPQNI SEVSTSL QKIQVRVLSI
26604	56972	A	26754	3	556	
26605	56973	A	26755	143	724	GWIPSDNSICVQEDCRIPQIEDA EIHNKTYRHGEKLITCHEGFKI RYPDLHNMVSLCRDDGTWNN LPICQGCCLRPASSNGYVNIYEL QTSFPVGTVISYRCFPGFKLDGS AYLECLQNL IWRPAHPGALLW KEEDLNIFLSFSISHTSGWQLLC FIFALC*SPLPPQHLPVQ LAPP LCSKCCSPA IKDV
26606	56974	A	26756	3	1393	CLRPASSNGYVNISELQTSFPV GTVISYRCFPGFKLDGSAYLEC LQNL I WSSPPRCLALEVKIPVS GAVRVITL PVTLGHPNVVTQR WKAGASDKGELVVLKLLFSPT AQVCPLPPMVSHGDFVCHPRPC ERYNHGT VVEFYCDPGYSLTSD YKYITCQYGEWFPSYQVYCIKS EQTWPSTHETLLTTWKIVAF TSVLLVLLLVILARMFQTKFKA HFPPRGPPRSSSDP D FVVVDG VPVMLPSYDEAVSGG I SALGP GYMASVGQGCPLPVDDHSPPA YPGSGDTDTGPGES*TCDSVSG SSELLQRLYSPPRCQESTHPASD NPDI IASTAEVASTNPGIDIAD VDSNKLDPDWTQKYRVASPAR STCEDRSGAPVGT HESLFFSIPS SARQDWAPLDSQLESPQCR LPT LQRDFLVD PQAERPVLDP ELT ETWCNPNKRIERHMEHSGIEA

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26607	56975	A	26758	1	500	
26608	56976	B	26759	19	148	
26609	56977	A	26760	184	539	LPAKEEEGHKSKSGPLLGPARRA LPGTALGARGAEQGDPEADH* GADTTKRCPLGPAPVPRKGIP AEGPRRGRAGLGMWGPGLGA HRTAAPSPAEAPSPCQHPSSHSC PVACFEPVF
26610	56978	A	26761	1	441	DENRELLGVELDGIDVLIQLSV FKRHNPFSTAEQEMMENLFDLS CSCLMLSSNRERFLKGEGQLM NLMLREKKISRSSAL/KVL/DHA MIGPEGTDNCH*VCLTFLALR/T IFPLFMKSPRIKKVGTTEKEHE EQCCSILASLLRN
26611	56979	A	26762	1	2403	
26612	56980	A	26763	17	751	AKMPFDANKLYCSEVLAIFFS PLENRELLGELDGIDVLVFA*Q VFKRHNPFSTAEQEMMENLFD SLCSCLMLSSNRERFLKGEGLO LTLL*LSHSSDCEMPTWRGGS MEQGGRMGLGLVSVGLEHALL LTYGLYQRLPPQPQNAQPSFVH REKKISRSSAL/KVL/DHAMIGPE GTDNCHKFVDILGLRTIFPLFM KSPRIKKVGTTLPLPAAATPT NRPSAMNGRVRMEAEQSSAHC

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26613	56981	A	26764	1	1914	MAEGERGADVPH/GPRGLAGR RGVVGGAARGRAG/PGGT/EGGG GPESLGGSGVGDSSGGCAGPP SAPPARRRVPLAMGPRNLLIDW IWIMDTTLGLGTEGGHSPVVL PLCASVSLLGGLTFGYELAVISG ALLPLQLDFGLSCLEQEFVLVS LLLALLASLVGGFLIDCYGRK QAILGSNLVLLAGSLTLGLAGS LAWLVLGRAVVGFALSSMA CCIVVSELVGPRGRVLSLYE AGITVGILLSYALNYALAGTPW GWRHMFGWATAPAVLQSLSL FLPAGTDEATHKDLIPLQGG APKLGPRPRYSFLDLFRARDN MRGRTTVGLGLVLFQQLTGQP NVLCYASTIFSSVGFHGSSAV LASVGLGAVKVAATLTAMGLV DRAGRALLLAGCALMALSVS GIGLVSFVPMDSGPSCLAVPN ATGQTGLPGDSGLLDSSLPPIP RTNEDQREPILSTAKTKPHPRS GDPSAPPRLALSSALPGPPLPAR GHALLRWTALLCLMVFSAFS FGFGPVTWLVLSIYPVEIRGRA FAFCNSFNWAANLFISLSFLDLI GTIGLSWTFLLYGLTAVLGLGFI YLFVPETKQGS LAEIDQFQKR RFTLSFGHRQNSTGIPYSRIEISA
26614	56982	A	26765	201	632	NLLLCPLSAESRPEEGVRLFCSC FRSRQRPQAHKSAWGTTALSES MNCFA5FGASISSADQEQHLHL PGAVGSGRPGEC LGPSGRCSK* GATFPQKGRWKEARPSVPVAP AAGLQSRAGHPRGIRPGRPHG ERDSACWGR
26615	56983	A	26766	197	777	LPSRGAGLRTCSPCLSLPPTPW TPVRPEPPQARAPPTPRRPVPS TQGLRNASARRGTGR/PAPP/VS PGAGSTRIEASWAPESAARAGL WGPSNSVQRAAESASRPHFG QPPKAPARPGWLTKGFASVPS ASRRAPPAAVTSARHYLVRQPP PRPSSCPECNKIRLWPAFQLTPL CQGPAASEDRRKPQKRR

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26616	56984	A	26767	178	697	ATLFIQKHQSGVKSTNP*IGRRS LTPEITAELGLERLNPRRCSSCL LGLKFEYHNSNLPLQLHGGQAC GDPTNSVQRAAESASRPHGFGQ PPKAPARPGWLTGKFPASVPSA SRRAPPAAVTSARHYLRLQPPPP RPSSCPECNTIRLWPAFQLTPLC QGPAASERDRRKPOKRR
26617	56985	A	26768	1	858	
26618	56986	A	26769	10	1332	
26619	56987	A	26770	1	1086	
26620	56988	A	26771	1	1392	
26621	56989	A	26772	1	987	
26622	56990	A	26773	1	336	
26623	56991	A	26774	46	302	APGAVKKTWFGKKGREKQGE RR*RQLGKENENIVALQLIRTD QEYWRHHSWHFFLSAAACQPE LFLKKHTAKNNRRJRVSQKWK
26624	56992	A	26775	1	1839	
26625	56993	A	26776	284	816	APGAVKKTWFGKKGREGETR EKNNQPTVRTNSQTRDTFFKT* DLF*RMPSWELSPASS*ASKTI KYLGIQLTRDVKDLFEKYYKTL LNKIKEDTNKWNIPCSRIGIINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPPEAAEQQLPN SQSCYLIPLLEASSQSGSWLY

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26626	56994	A	26777	1	2547	MVKGSIQQEELTILNIYAPNTG APRFKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSKEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSOLKELEKQEQTHSKASRRQE ITKIREELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDIITDPTIEQT TIREYYKHLYANKLENLEEMD TFLDYTYLPRLNQEEVESLNRP TGSEIVAIINSLPTKKSPGPDGLT AEFYQRYKEELVPFLKLFQSI KEGILPNSFYEASIIIPKGRDT TKKENFRPISLMNIDTKILNKIL ANRIQQHIKKLIHQDVGFIPG MQGWENIRKSINVIQHINRAKD KNHMIISIDA EKA FDNIIQQPFML KTLNKLIGDITYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTTRQ GCPLSPLLFNIVLEVLARAIQ KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLIISNFSK VSGYKINVQKSAFLYTNNRQ TESQIMSELPFTIASKRKYLG QLTRDVKDLFKENYKPLLKEIK EDTNKWKNPCSWVGRINIMK
26627	56995	A	26778	1	489	SISWKLWFTEFTLFRFFQPSVSA VPVSTLAVVLGLKTL SLLFSHSF PGRHSWALRAISLLPSFLYTSSL MNSFSYTVHLYLGGLLRLCGSR DPHACGFPEGSPLPSCSAA*PFI WGMKRPSCVLAPSCSRDSFG CLFSFGHQCLHKSHVGSPPSGP ERLYNG
26628	56996	A	26779	354	685	YRGYLRGECFP*KALCCEPAAY LQTCNPFSPGACSGHALHSLN VGDCVYLICPRYPPLRRAGKPR DTGIEGRTLSSGGPSVHSSFHSA VLPFPYTSKLLWIERRRPAGQS
26629	56997	C	26780	1	867	
26630	56998	A	26781	139	513	
26631	56999	C	26782	1	948	
26632	57000	A	26783	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCR*PYSRGT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
26633	57001	A	26784	1	224	SRAGYDHHVVEPVERGTSGVVRW YACCGLMVCPANPQHFAHGY/ VGKIPGYPARAGTLTGLHPMQ VCRRCRCVYEI
26634	57002	A	26785	112	254	
26635	57003	C	26786	1	567	
26636	57004	C	26787	1	543	
26637	57005	A	26788	165	633	RIPGLLLCPAYPQHFAHGYVDK IPGYPGRI GTLTGLHPMQVCR RRQAPCMKSNALIVILGTVTL DAVGGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDFRGRRPVLLASLLG ATIDYAIMATTPLWYPLVNS
26638	57006	A	26789	264	800	ISNFELCSRSIHLLCSSTGYPR AGTLTGLHPMQVCRRCR*PAV
26639	57007	A	26790	1	738	
26640	57008	A	26791	84	162	AVLDLGPPTGRDPPQGSPPDYS GAFLASCAGAPLQQRQRKEQ AAIFAVLQLLVIPPGVGGTQT NRVWSGFANHGPNPGYPGRAG TLTGLHPMQVCRRCR*PPYRVI PQCGTLPQQGQPEVFVKQFWIL GLRLGETPHRGHQLIQGHSC
26641	57009	C	26792	1	531	
26642	57010	A	26793	216	519	QRESTIPSRPVERSNLGVRLYAC CGLLLCPAYRQHFAHGYVDKIP GYPGRAGTLTGLHPMQVCRRCR R*PDRRGTERVSARKHVCVFFV SLFVAACRPPLRA
26643	57011	C	26794	1	606	
26644	57012	C	26795	1	1059	
26645	57013	A	26796	1	3285	
26646	57014	C	26797	1	1390	
26647	57015	A	26798	211	679	RIFKCKADLLYDMLVYVTLWI HRAVTYTHRVNHSYRRSNIKS ETTVPTIRIVGPVERSNLGVRLY ACCGLLCPAYPQHFAHGYVD KIPGYPGRAGTLTGLHPMQVCR RCR*PKPAPLPGSPQHLCSHQPH LAQRKTGQCFLQGHCFPEKNW GTIV
26648	57016	C	26799	1	774	

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26649	57017	A	26800	542	1269	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQRKYP GCRLYASCELLLCPVNPQHFAH GYVDKIIPGYPAGAGTTLGLHP MQVCRRCRRQAPCMKSNNALIV ILGTVTLDAVGIGLVMPVLPGL LRDIVHSDSIASHYGVLLALYA LMQFLCAPVLGALSDRFGRRPV LLASLLGATIDYAIMATTPVLW
26650	57018	B	26801	1	1531	
26651	57019	A	26802	1889	2154	
26652	57020	A	26803	147	162	APSLHLKDTVDRSNLGVRLYA CCGLLLCPAYPQHFAHGYYVDKI PGYPGRAGTLTGLHPMQVCRC RR*PGAHTVVDIRPREDHLGSA GQPNCPENGCLQGFTHTGLAYPE HHPCI
26653	57021	A	26804	2381	3641	
26654	57022	A	26805	1	2367	
26655	57023	A	26806	1	488	MDLLYMAAAYMMGLAAIGAA IGIGILGGKFLEGAARQPDLIPL RTQFFIVMGLVDAIPMIAAIAFV LFVLFCMKYVWPPLMAAIEKR QKEIADGLSSAERAHKDLVLAK ASATDQLKKAKAEAQVIEQAN KRRSQILDEAKA*GRQEPLVQV FLESARKR

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26656	57024	A	26807	2125	2435	VSPRQKSARPDLT*IRTLCKVL GVLFVAVGGKGPTCILQILKG QRRQEA*GISVMAERVWASGQ A*WEVWLHWAKSIDWFLFWK QHVHALRVRLDTCLFSLGESS FWNQGLTWKVVRRTFSESINH TPRITLGVPPSVHGIQLPGLLNF GEFKVCFVLSPRIFNLTHENFLS SEGPERRGLLGATFNCLNKRRLA KYRMNRNVHPKPLRVYLHSRL PPEPAAAP*A WCGPRHLSRRQM SSSSQIGNDSFQLQVTPVHLLPL SHTTRKNPEMYDLPLLIINPQES AILQLFHQDGECLHCSPIVGDW CHLGHSQACPSFHVPSGLFVPS LLCGAAFGRLVANVLKRY SVC VRVCAHVHVCAVRVYACVC VRMTISLTVILIESTNEITYGLPI MVTLMVSTLPPGPCQAQGHVR PTGPFRSLLEWETEVEMDK*G HDFAHVLVSECISSSEA*GMLLL GGGPDRLSLESTFRAVWSLSRL DSVIAAGKQ*A*RT*SVGYSL CPDLKGDPASAVFILRTTVHHAF PVVTENRNGNEKFMKGNQJLISN NIKFKVKKTA*EERQVRDKRSR LTRLALPIRNMCDEDIASEPA EKEDLLQQMLERR*EPGGAPTA RRATQRWGEPLAQML*LTFFHG LILRSQVLVTLVRGVCYSESQS VSLSEAEISQARPDEARGVGRC RRADLTLLNPRMIVVRAAPAC
26657	57025	A	26808	24	369	
26658	57026	A	26809	4	371	
26659	57027	A	26810	82	703	
26660	57028	A	26812	1	1692	
26661	57029	A	26813	293	563	NVWPSSSVRGRNE*GREGRR RTQQAAGLGPAPSDLWWLWLS WCLQKNMSQGGENLPAGPGSC CGREAQEGAGTSLEDAFFFEAQ LLQLH
26662	57030	A	26814	1	488	VARLYWKRP SLHACHFRDPRA GLSENPRLLQCS PSSSSGNVWG PHLYAVPCL*NGRIIPSPWNYRS LNSITTSSTCSSFAVSSSPCPVW QLPGSCLLSRSLLRVAWSQAP VPMRSEQDQLQKPPPSAGLPA SVHANL*PGDRKGSVWTFAGV AQIPSPWP
26663	57031	B	26815	51	90	

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26664	57032	A	26816	299	707	RPPCRISCHPHTRCEGGRLRSRS PLLS*MPLSHPGPSQPPAGSMS SSPPATTSTCSCSPPAAGCTRGR TTGRPFWTASGPAELDWASGSS VGL*SQGSQGLGACGASYAGLG VPPRLLGPMTSCCMSLPFPSPAR P
26665	57033	A	26817	146	330	TVARRMELTPALLRALLNGILPI SEPPSNRIFACWGKPAWTACCN SLRARR*RAISCCPSH
26666	57034	A	26818	1326	1694	IFGWFGACCSLGSCCVFTAST CTTVCGGCAIKVGSCLSLATMG CCVCTSGLGCACSCWGVF* CLMESWGICSLCWSWSACRW MVCFLVWKHCRVFTCS*VCS SGGWLSFCCLADCD
26667	57035	A	26819	1	1407	
26668	57036	A	26820	75	1397	SRGSGREKFPAQLSYQTLTGKG PIEGTSLSNLAQQRCKEHHCHF LREQGPNCLIIERFMDRYTGKVI HMASHTTTRCPHVSRRPKARLL APATRSRSARARLRETRVRRGS PSCLLWLNRRSLPAEHSVRSPP RDMVFESLGLPSTKSSEFRSAA PEAAERAQPGDPCGLQTPAPLR PGFRRNQDPASAAAAAEVRS GGGRGRILATTLWGCNLTLCITQ YTRIRKLTLYVYCGVESKQEWG EYHEGVQAGLTRPGRSPKLISK FLEKELTDNRWDQDEAEAEVK SSFPKND*VLKNRAIKKAKRRN VGFEVSAPLQLLLFGGLVVPFG GGRFSGFGSGAGGKPLEGLSNG NNITSAPPFASAKAADPKVAF GK*LPSPSRLVDKVSNNKTNG DSQQPSSSGLASSKACVGNAYH KQLAALNCSVRDWIVKIHVNTN
26669	57037	A	26821	3	89	AASGRSFRGYSRRHCYHRR*QL HACHCP
26670	57038	A	26822	150	383	LCLGEVWKGFFLTGTGRPGVF LSLHKKACYHHNHRYHHHH HHQTKP*QQELNSLLHFPPHQI QGDQFHHLYYL
26671	57039	A	26823	105	417	LCLGEVWKGFFLTGTGRPGVF LSLHKKACYHHNHRYHHHH HHQTKP*QQELNCENMPQYNF QNGSQSYQTLTLL/SLSTKFM*YS KFFVVISVMFIASSPETDF

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26672	57040	A	26824	89	554	AMNSCVTGDYRSPCGGFGFAF LYSSVSVSSSEYQLSPLPPAKR PLAAQQSCSIPIASVFFQTIHSLF AKDKKEFSSNLLDSKVNMCHE AHQLISHS*ANFRSICHIPQRW* NLIFEKFSVDVSMGSGITG**AEN WS*TLISIAASLVYSLLHKKIQ
26673	57041	A	26825	84	239	ACTKKACYHHNHRYHHHHHH HQTKP*QQELNSFRFSLSPQLL AVFLFLRP
26674	57042	A	26826	2	245	
26675	57043	A	26827	154	546	LIVTVHVNHLGVLINHRFRISGC GVCGTDCISHKFPGAADATGPS WTHCAVITFSLTTGSATKKTE DNNTFVFNVVDVKAN*HQITRA VKKLCDIDVPEVNTLPNVISIFR FLCSTVFCTLTVFFLRENG
26676	57044	A	26828	331	612	NHRGLFPDPYIPGTYFLFFFLF FSFSSSSSSSFPASGNNHNTLY FYGINFFSFHIGMRMGIFLCLT CFT*HDVLQAHPHREGRQDLLF HD
26677	57045	B	26829	928	1617	
26678	57046	A	26830	95	929	
26679	57047	A	26831	3	1128	LYNRRRRRRCSCRHRCRLSS GLRKEEVISLGASLGRVFPVPCSP PTVSAARGPTGAPGGPNSKPLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNLVEILP AIFSSFLNLQHVNLWFLAAM KAVTEQGHELSNEERNLLSVA YKNVVGARRSSWRVSSIEQKT ERNEKKQQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKRLSNYFRLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFLTILIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTLCL DI*P*QNSACVINFLNLNLRDN LTVSTTSTGFIVSFLFTYLIHCHY LQEVCSVSLCTLNIYPLCDKCK
26680	57048	A	26832	139	601	EGRGHLAQELLSEVFPVPCSP TGMTMDKSELVQKAKLAEQAE RYDDMACSSERHVTQGHLS NEEKKSCSLVAYKECW*APRR SSWRVSSIEQKTERNVEGSSR WGKEYREKIEAELQDICNDVL ELLDKYLIPNATQPSKVFYLYK MK
26681	57049	A	26833	70	122	

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26682	57050	A	26834	179	876	CIVILFFFSQFNFVGRILGPRGLT ANVNRYLELHLYGYMNLFI SIMKDVLSL*RE*F*SCTL*IF*E EQNRGKPNWEHLNEDLHVLIT VEGV*I*LLYLWTVSNAFISCVF HV*AEGEDRYCCLYTFS*ISLLT VAALAFSLAATAQAAPRIITGP APVLPPAALRTPTPAGPTIMPLI RQIQTAVMPPNGTPHPTAAIVPP GPEAGLIYTPYIYIISKYLLSS CSPEP
26683	57051	A	26835	3	915	AEAHPLRPDAADERQEAHDSLP NFCGIFNHLERLLDEEISRVKRD MYNDTLNGSTEKRSALPDV GPVQLQEKLYVPVKEYPDFNF VGRILGPRGLTAKQLEAETGCK IMVRGKGSMDKKKEQNRG/ KPNWEHLNEDLHVLITV/EKV LQEQGQEIKKRAVEEVKKLLV PAAEGEDSLKKMHLMLAILN GTYRDANIKSPSLAFLAGTAQ AAPRIITGPAPGLPPAALGTPTP AGPTIMALIRQIQGTGGMNGTP HPTAAIVPAGPEAGLRYTPYEY PYTLAIPATSILEYPIEPSGCI
26684	57052	A	26836	1182	1360	KLSCVYIYICMFHYTHVSV*FYI YIYTHRHTENHYFCNSVQFVLY LFTFFCYFIWPA
26685	57053	A	26837	3	348	RNSKHVCRAEP*GHFCYK*HF WNHTEHTAVLEI/EQINARDET DFYLGNRCTYVCKEQHSGPGS KSNTTIVIWGVTCQAQKNSV VCAKFSQHPKAKIGHRIHVML YHWRIQH
26686	57054	A	26838	264	527	NSKHVCRAVP*GHFC*K*HFV NQREHTTVLEIEGVYARDETEF YLGNRCTYVCKEQHSGPGSKS NKTRVWIKERGSGWCRLSGR
26687	57055	B	26839	26	515	
26688	57056	A	26840	92	341	
26689	57057	A	26841	224	1111	
26690	57058	A	26842	2	592	HSLTGRCIFFLITGTPSGPEMST TLKIMSSKEPSISPEIRSTVRNSP WKTPTETTVPMETTVEPVTFSPQ LVFARLMTGVGLGAALPNLIAL TSEAAGPRFRGTAVSLMYCGV PIGAALAATLGFAGANLAWQT VFVWGGVVPILVPLLMRWLP ESAVFAWRSISNKA*FRDCRC CSAAIHW*RRFPFKSKPVM
26691	57059	A	26843	2	141	

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26692	57060	A	26844	1	978	
26693	57061	A	26845	144	647	
26694	57062	A	26846	1642	2652	FGILVLLALIVIWYNNFFGAETE AILPYDQYMHFFAAVYFQQGNM ESNGKYVDRNGNVVDYQTGPIL WGEPTNGQHAFYQLIHGQTK MVPCDFIAPATHNPLSDHHQK LLSNFFAQTEALAFGKSREVVE QEYRDQGGKDPATLDYVVPFKV FEGNRPTK*ILLREITPFSKLENE KAISDTICVIRDGQHGTRDGIE HLTAWHPVNRHIKRVNDVSFS LKRGEILGIAGLVGAGRTETIQ LFGVWPGQWEGKIYIDGKQVD IRNCQQAIAQGIAMVPEDRKR GIVPVMAVGKNITLAALNKFTG GISQLDDAAEQKCILSHPRCSW QGRHLLH
26695	57063	A	26847	52	137	
26696	57064	A	26848	1	1858	MGLKVDDKVLFAVVSRLTSQ KGLDLVLEALPGLLEQGGQLA LLGAGDPVLQEGFLAAAAYEP GQGVGQIGYHEAFSHRIMGGA DVILVPSRFPCGLTQLYGLKY GTLPLVRRTGGLADTVSDCSLE NLADGVASGFVFEDSNAWSLL RAIRRAFVLCQGQFHHRTTDVE YKGDPAVKIEESEINYLNNVY NTHFFKKQLSRDDIVWTYSGVR PLCDDDESQPAITRDYTLDIHD ENGKAPLLSVFGGKLTTRYKLA EHALEKLTPYYQGIGPAWTKES VLPGGAIEGDRDDYAAARLRR YPFLTESLARHYARTYGSNQRA ACSAMREREARTLPQKLAGTL GMLSKVMRIPRQEVTAALRTY LQIRIGLHAAFNACEEMCQRVA LERQLDSEERALLIERSQTVIRQ GRDLLHAWDATWNSAQLDN ALQPDRAQGFADALEKYAADE SFFAQLDKYDIPVVVIGKVEGQ YAHVYSVDTDNFGDSIALTDAL IESGHQNIACLHAPLDVHVSVD RVNGYKQSLAAHNIAVRDEWI VDGGYTHETALKAAARQLLSQS PLPEAVFATDSLKLMSIYRAAA EKNIAIPQQLAVRILFGLHL*IV LSTRAGFNGLAHY

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26697	57065	A	26849	136	3261	PMSPTIYDIARVAGVSKSTVSR VLNKQTNISPEAREKVLRAIEEL QYQPNKLARALTSSGFDAIMVI STRSTKTTAGNPFLLEVAQAFP AKAE*KGQVLVRTSHNPAEDL KKCESKIKQKMIKGIIMLSSPAD ESFFAQLDKYDIPVVVIGKVEG QYAHVYSVDTDNFGDSIALTD ALIESGHQNIACLHAPLDVHVS VDRVNGYKQSLGAHNIARDE WIVDGGYTHETALKAAARQLLS QSVLSLVAVWSWAC
26698	57066	A	26850	73	174	
26699	57067	A	26851	252	575	PGFPRGPPPPGFAFFHVISWDT DLSDDPAARAGLGVWRTPDPPR RAARSPVLRPLSAGQRPAAARL LGGMEEGFRQVAVFSES*SAV CPPSPPPPLSPLAPWTETA
26700	57068	A	26852	1	462	AQSVNSQTFSELRAQTQIFVKTT SHNSPGVFHTSTKR/FIDGNPPGI FSAITA*RLMMP*RSSIFSASASI LSVSFSGSTCNNDQRPARFGVL *DTRGETGCA*TGRPRAR*LR RVEVRV*LLRVRRARNGAQMA LVKTPCQTSAHNAPCRGRE
26701	57069	A	26853	692	918	
26702	57070	A	26854	1	2427	
26703	57071	A	26855	1347	1978	LPHCVANHGICALR*QKWVHD KEQTTQTLKMAENGRWVIDD IVSNHGSVLQAVNSNEKTLAA LASLQKEQPEAFVAELFEHIAD YSWPWTWVSDSYRQAVNAF YKTTFTKANNPDEDMQIERQFI YDNPICFGEESLSRVDEIRVLE KTADSARIHVRFRTLNGNNEEQ ELVLQRREGKWEIADFIRPNSG SLLKQIEAKTAARLKQ
26704	57072	A	26856	1	733	LSEVDVDVRQSIHSAHAKTLD QGLRNEFLVEKVFADEYTMV YSHIDRIHVGIMPTIKTVSVGG EVGKQLGVSYFLTNSRRITNKY LVPDVLETCQSSMGLTELAPGN *WNTMPCHTHERMEVYFYFN MDDDACVFHMMGQPQETRIH VMHNEQAVISPSWSIHSVGVTGK AYTFIWGMVGENQVFDMDMDH VAVKDLRANHHRFIHSQRSDI HLTTQWIKRAAQTIHPPVSIIQQ IVAFFE
26705	57073	A	26857	2	255	
26706	57074	A	26858	1	597	

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26707	57075	A	26859	2	640	EARGRQQLHHLPHPHPRASSP LALQPLGRSRCPPPGAAAPD PRPDMGDLPLGLVRLSIALRIQPN DGPVFKVDGQRFGQNRRTIKLL TGSSYKVEVKIKPSTLQVENISI GGVLGPLELKSKEPDGDRAVY TGTYDTEGVTPTKSGERQPIQI TMPFTDIGTFETVWQVKFYNY HKRDHCQWGSPFSVIEYECKPN ETRSLMWWNVKESFL
26708	57076	A	26860	218	426	TQPRVWSQAQ/RALQPDTELPQ PPQTPKSDTDQMLSVKKKKKKR KKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKLYFQT
26709	57077	A	26861	1	423	
26710	57078	B	26862	I	252	
26711	57079	A	26863	1	171	
26712	57080	A	26864	5	254	
26713	57081	A	26865	16	220	ILDTPSMRWTKNFMSILAQPE QQCKTLSONKNDRRIKKKEE KKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKEKE EEKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK KKK
26714	57082	A	26866	32	286	
26715	57083	A	26867	1	847	EVKDLYDKTFKSLKKEIKEDLR RWKDLPCSWGRINIVKMAILP KAIYRFNAIPIKIPTQFFNELEGA ICKFIWNKKPRIAKTLTKDKR TSGGITMPDLKLYRAIVIKTA WYWYRDRQVDQWNRIDPEM NPHTYGHILFDKGAKTQWKK DSIFNNWCWHNWLSCRMRRI DPYLSPECTVKSKWIKELHIK ETLKLIIEKVGSLEDMGTER FLNRTAMACSKKKEKEKEEED EEEEKEKEKEKEKEKEEKK KKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK
26716	57084	A	26868	1	376	MLMKDPQWNSSIFSTHIALQQL KRRQAIEYGAQEPSRRIVGGKGS GAQVDEEEEEEEEEKEEKK KKKEKRRKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKMLL LSLPMIRPLPHRWASSPSSMV AKP
26717	57085	A	26869	1	2031	
26718	57086	A	26870	1	957	

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26719	57087	A	26871	171	495	SQLLDMRKPFQKPGRLQLKTL P QYLNTR/CILDYLDN/SPQQIRK LFYVLSTLAFSKQNEASSHIQD DMHLVIRKQLSSTVFKYKLIGII GAVTMAGIMAADRSSEPSL
26720	57088	A	26872	1	3114	
26721	57089	A	26873	173	397	
26722	57090	A	26875	823	1194	
26723	57091	A	26876	1	1263	MESNAVQLTRMEYAMKSLSL YPKSLSRHVSVRTSVVTQQLS EPSPKAPRARPCRVSTADRSVR KGIMAYSLEDLLKVRDTLML ADKPPFLVLEEDGTTVETEEYF QALAGDTVFMVLQKGQKWQP PSEQGT*WRRTRQKDSVPSRPC STHGLQEIQ
26724	57092	A	26877	128	317	
26725	57093	A	26878	431	574	
26726	57094	A	26879	112	482	EGPEAKPKRSNCAPEKRSSPIPD WEPAFSEDGRARTVARLQHPPL GGPTHRYHHFLRRHDPLRVHP AAERQEAHPGTST*QSSPNSKQS PQGWKWTFFNSSLSTRKYVYFQ QPRGWDFFKKT
26727	57095	A	26880	3	179	
26728	57096	A	26881	977	1127	
26729	57097	A	26882	121	708	
26730	57098	A	26883	38	828	GSRLRLQAAAAFPALPLPLPP WEWKHLPHVPEAKWWLTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESLDLAEFAK KQPWWRLFGQESGPSAEKYS VATQLFIGGVTGWCTGFIFQKV GKLAATACGEVDF/LLQLANH TWVHQSLTGNEWKDIEESPKS SLKIRKSQSDYLLRSGAKAAGC WCHFVKKNVLVTWGIFPEAFC LAWHPKEDDLHVPLFPGFFPSQ QPFTLHHRDIESLLFFWPWPSF GHWEN
26731	57099	A	26884	1	642	
26732	57100	A	26885	1183	1349	

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26733	57101	A	26886	1	1371	MSFLIDSSIMITSQILFFGFGWLF FMRQLFKDYEIRQYVVQVFSV TFAFSCTMFELIIFELGLNSSS RYFHWKMNLCVILLIL/VFPMV PFLQLAYFIVSNIRLLAHKQRLLF SCLLWLTFFMYFFWKLGDPPIL SPKHGILSIEQLISRVGIVGVTL MALLSGFGAVNCPYTYMSYFL RNVTDTDILALERLLQTMDMI ISKKKRMA MARRTMFQKGEVH NKPSGFWGMKSVTTSASGSEN LTLIQEVDAALEELSRQLFLETA DL YATKERIEYSKTFKGKYFNF LGYFFSIYCVWKIFMATINIVFD RVGKTDPTVTRGIEITVNYLGIQF DVKFWSQHISFILVGHIVTSIRG LLITLTKFFYAISSSKSSNVIVLL LAQIMGMFYFVSVLLIRMSMPL EYRTIITEVLGELQFNFYHRWF DVIFLVSA LSSILFLYLAHKQAP
26734	57102	A	26887	1738	2140	
26735	57103	A	26888	81	733	
26736	57104	A	26889	1061	1154	
26737	57105	A	26890	1	3207	
26738	57106	A	26891	113	367	
26739	57107	A	26892	2	1391	
26740	57108	A	26893	154	647	
26741	57109	A	26894	40	747	
26742	57110	A	26895	1	3186	
26743	57111	A	26896	271	491	
26744	57112	A	26897	304	1836	
26745	57113	A	26898	1	2343	
26746	57114	A	26899	1	765	
26747	57115	A	26900	318	473	
26748	57116	A	26901	2	426	
26749	57117	A	26902	1	433	
26750	57118	A	26903	2	1004	
26751	57119	A	26904	125	199	
26752	57120	A	26905	3	156	
26753	57121	A	26906	2	397	VDGMGWSQDLFRALGRSLSR GKEHVGTQDFGNKY*SRSTK TGEVRWRRGQRLRGQ*LRGQT IREKRIVEAANKKEVDYEAGDI PTEWEAWIKRTRKTPPFMEIIL KNEKHREEIKIKSQDFYEKEKL
26754	57122	A	26907	1	1350	
26755	57123	A	26908	1	582	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
26756	57124	A	26909	2	687	GARQVLPGESPCFSSVAKIVKP NGEKPDEFESG/LSPQALLELAE MNSDLKAQLREPELLRPA*GK LKVGCSSENLS/ILLFPVPSN*K SFPENPVQRA*YRELEKKFQW GSHVGLYRPQRRILP*AQLRKK PVQKNKQKASPRARLTAVHD AILEDLGLPQAKIVGARESRVK LDGSRVAKVHLDKAQQNNVE HKVETFSGVYK/KLTGKDVNF EFPRSFNCKQK
26757	57125	C	26910	164	208	
26758	57126	A	26911	2288	2625	GSEGLHPITKRWSSLWEWRKG LSEVGSCKRNLRCLRTAI/LM GGEAGVIHCKGHQKASDPALG NAYADKVARQAASSPTSVPHG QFFSFTLVTPITYSPAETSTYQSL PTQ GK
26759	57127	A	26912	1	400	
26760	57128	A	26913	3	277	
26761	57129	A	26914	1	630	CEIKNRKAAEKVNKTGKGFEEI NTYPGPIKTGPGSQTKWLDI VRNLTVEEDTSSWSVRAHQPK STLTGTGRPSTNGTMSSSLARTV REEPGNQPNYRGKPSFWFPHL VRAASTQPVITRLLQHGRKLP NSPYNFPILPVLKPKDKPYKL VQDLHLINQIVLIHPVVPNPYTLL SSIPASTTHYSVLDLKHAFFTIPL HP*FQPLFTF
26762	57130	A	26915	1	384	
26763	57131	A	26916	1113	1319	GRDPVSFAFYIWLASFNTIY*IG NPFPIACFSQVCQSRSDSCRYAA LFLRALFCSIDLFLCFTSTMLF
26764	57132	A	26917	2	2144	
26765	57133	A	26918	99	470	
26766	57134	A	26919	636	1220	GPGFQAQNCAAIWADTKLAAG IFSHTPVAPGTPVRQNHLLPWD APAWSGEECLPLRLVYVVPFS QCKQSCQEV*TGQSPPLGKAF VARLPL*IPSLWAGHLFLEHPV YCCGCVTAGRQGSWKQRRH GHFPPLPLLLQMVCCSISYQY DYPESSFLLLFLSSLCSAGKSTG SHAILLSAFVLPHLVALRS
26767	57135	A	26920	10	161	RLRMVRDIKVLNTRSLRNCIG DLTNKGRSIIIGPPL*ELSKASVM VPVGF
26768	57136	A	26921	1	855	
26769	57137	A	26922	5	1442	
26770	57138	A	26923	1061	2332	

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26771	57139	A	26924	804	1100	SPKGGPPDPSPHGTGKFIHSRPEET TKQAACEQHGCLFHLGTLGALL G*QRWLHLQSRPSLGCNENKSL FQ*PPLP*E*KEIQCKVPPNLGL GVRSGKGF
26772	57140	A	26925	3	1186	
26773	57141	A	26926	126	363	SRSKQDGLDPSGTWCKRAFSPG PWPIIPVAAGGGHSGGGKSET PAHLQKGLHKVKNK*PSTYSVC QTPDAEHPVSNK
26774	57142	A	26927	1	1125	
26775	57143	A	26928	401	446	
26776	57144	A	26929	332	499	
26777	57145	A	26930	74	200	
26778	57146	A	26931	300	416	
26779	57147	A	26932	324	430	
26780	57148	A	26933	60	381	
26781	57149	A	26934	2344	2453	
26782	57150	A	26935	131	274	
26783	57151	A	26936	144	444	GGGENFSYPWYLLVCGWFFSS SPIVPDVPFSLLLPAQKKKPPAP PKPEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK
26784	57152	A	26937	540	811	
26785	57153	A	26938	69	375	QHLPAAVAAATMPKKAEGD AKGDKAKVKDEPQRRSARLSA KPAAPPKPEPKKAPAKKGEKV PKGKKGKADAGKEGNNPAEN GDAKTDQAQKAEGAGDAK
26786	57154	A	26939	9294	9486	SLLYQPRCMAFRIKASS*RGMP GGSASAARKPTG/SPGREGAGR RGQWGPNNCCAGRLPGGESTV
26787	57155	A	26940	248	613	
26788	57156	C	26941	94	234	
26789	57157	A	26942	2157	2408	
26790	57158	A	26943	547	815	
26791	57159	A	26944	254	467	VFLISVYNGLAISLYLGIHQRK PVMRPNPLNCFGLV*G*AGIG *IRSSLRTLVLDFNSPKYLTF EQS
26792	57160	A	26945	238	391	
26793	57161	A	26946	232	1659	
26794	57162	A	26947	1	951	
26795	57163	A	26948	1	2046	
26796	57164	A	26949	3	97	SVR/SKFYVREPPNAKPDWLKV GFTLSVEL*M
26797	57165	A	26950	1	828	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US\$N 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
26798	57166	A	26951	224	475	AGPRKMAPSALLRPLSRLLAPAR/LPSGSPVR/STKFFVREPPNAK/PDWLKVGFVLGTT/VFLWIY/LIKQHNEDILEYKRRNGLE
26799	57167	A	26952	1	411	
26800	57168	A	26953	442	2490	
26801	57169	A	26954	3	1592	
26802	57170	A	26955	9	308	
26803	57171	A	26956	153	227	
26804	57172	A	26957	1	411	
26805	57173	A	26958	517	825	
26806	57174	A	26959	6	646	
26807	57175	A	26960	1	275	
26808	57176	A	26961	3	272	
26809	57177	A	26962	1	1002	
26810	57178	A	26963	1	1791	
26811	57179	A	26964	2	160	HMTTSLLAQSGFQKTSALNKITTKGSH*VQFTSLPPPERVLVSMAERPWGG
26812	57180	A	26965	1	892	
26813	57181	A	26966	1	549	
26814	57182	A	26967	234	387	SCLEVCEQDGPEK/ITRQALRGVSSVTEDTLNICRLCWQPLPEPELWPKAL
26815	57183	A	26968	269	501	RARSEGAGLWSVVPASVSVFFVSDPRCAPFHRSPSCCSP/RRPCLSLSA*SRPRASGVGACLLWQPLPELELWPKAV
26816	57184	A	26969	210	296	
26817	57185	A	26970	71	283	LRLGDLPEINPLSSCSLLREKDPPTTSGPQTS/SPRNISPISNPDS/IGNRTVQLTWQPLPEPELWPKAL
26818	57186	A	26971	1112	1180	
26819	57187	A	26972	71	284	LILGDLPEIKPLPSCSLLREKEPPTTSGPQTS/SPRNISPISNPDS/IGNRTVQLTWQPLPEPELWPKAL
26820	57188	B	26973	1	663	
26821	57189	A	26974	1	502	MLLTQSLFGGLFTRTHMKFGAVTQIRGPPLGDKSPVLLLFALERQRRHVLMSMDPKLRCWSRTGKAFFPWCLIIAEMPDIYS/TFQRCTTQGRLPWSFTLSSKSRFSGEGARACYKCQKSDHQACECPQGIIPKPCICAG/PTGNRTVQLTWQPLPELELWPKAL
26822	57190	A	26975	233	496	
26823	57191	A	26976	226	543	
26824	57192	A	26977	1478	1744	

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26825	57193	A	26978	3	450	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHNLI LRPNPLCPHPDLVSLCPDPFPAF LEAHKNFQTTEPQQPGVPEPP PTGACYTCRKSGHWAKECPQP GIPPANHVPVWDPTENLTVQLT WQPLPEPELWPKAL
26826	57194	A	26979	615	724	
26827	57195	A	26980	1	1968	
26828	57196	A	26981	227	556	
26829	57197	A	26982	400	548	
26830	57198	A	26983	1	1968	
26831	57199	A	26984	65	741	
26832	57200	A	26985	1	658	
26833	57201	A	26986	1	666	
26834	57202	A	26987	67	608	NPGKGGCFVL/VLDGLLRDRKA VIREETFDGWHFPQDRPLPAHA\ LVAGIDRPTPPQK*TA\AMGKK KDRPKRSKIKSFCGKCYNY\NH\ LMPHKGTLWDIFLGQNLVQVL RDVFRDPSGLNRKA\REGPRF KFE/EREYETGQETKVVLPRLK AGFKNAFGFDSLKIHKKKKKK KKTTKKGRP
26835	57203	A	26988	1	352	
26836	57204	A	26989	1	1419	
26837	57205	A	26990	2	878	
26838	57206	B	26991	75	2931	
26839	57207	A	26992	229	724	IIFIVYSSQLTYVKISDSFQTFKF CLDFCLFFSEMS\FLSLNISSCS* YSAKVNSCGKFGLTGKSFSAPL TPLFFLCFSGSELVEGV*ELLAVG GLHLARIFLCLSISSLC*FTHSCS FTRVTPINLASNNSCLLGFRLQS SSIAPSLGLLDGGVCFIRDLAAA
26840	57208	A	26993	737	1048	KKYNIQLEKPYFKHLYKNKLL KLNS*NMITSVQQTIELEGNLS LSCIELVC/ILVTHCHLF/CMNK AW*QKKN/WSILTC*KHWQ YYNLVNSTDFNTSSSFLSKV
26841	57209	A	26994	1	1209	
26842	57210	A	26995	2	1683	
26843	57211	A	26996	1	1386	
26844	57212	A	26997	1	471	

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26845	57213	A	26998	2	514	VTARRRGTRWLRFRASRVQK WLVLDYFYLRYYVGHKGKFG HEFLEFEFRPDGKLRVANNHN YKNDVMIRKEAYVHKSVMEEEL KRIIDDSEITKVEDDALWPPDR VGRQLEIVIGDEHISFTISKIG SLIDVNQSKDPEGLRVFYVLVQ DLKCLVFSLIGLHFKIKPI
26846	57214	A	26999	1	570	
26847	57215	A	27000	1	980	
26848	57216	A	27001	270	356	
26849	57217	A	27002	1	1032	
26850	57218	A	27003	1	1017	
26851	57219	A	27004	1	450	
26852	57220	A	27005	1	637	APIECGGIPSLPVLQCSRANDQE GVRLLPESEAMPKSKELVSSSSS GSDSDSEVDKLLKRRKQVVAS ENPVKKQKTGETS/RALSS/SKQ SQPAARDNMFQIGKMRYVS VIRDFKRQKCLNDIREYWMDPE GEMKPGRKGSINP/QQWEPL KEQISGLPIDASKTKKISEPLI KPCTVPVVLWLFSGFCFLNVL RSYCMFGLQKNL
26853	57221	A	27006	20	412	RFSPLSFLLAGDSCTCAGSKCK KECKCTSCCKSKWDPLPLPLP CPPACPLSTILRGIAVWGCPA RKLLPPQ*SLSGRAGILPGVAS THLCRLLSAPRCCSCCPVGCAC CAQGCICKGASDKCSCCA
26854	57222	C	27007	32	505	
26855	57223	A	27008	854	1021	ALGGVAEYDLKEGLLLKH*AL VQSLVATEVRLVLCITSHDML QICFFVYATVQ
26856	57224	A	27009	1	726	
26857	57225	A	27010	99	537	
26858	57226	A	27011	1	963	
26859	57227	A	27012	146	609	VYLRCTGGEVGATSALAPKIGP LGLSPKKVGGDIKATGDWKG LRITVKLTQNRQAQIEVVPSAS ALIIKALKIEPPDRKKQKNIKH SGNITFDEIVNIARQMRHSLAR ELSGTIKEILGTAQSVGCNVDG RHPHDIIDDINSGAVECPAS
26860	57228	A	27013	3	501	
26861	57229	A	27014	1	1623	

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26862	57230	A	27015	53	1227	QPPVHTTPASSPCDDIDIAALIV VDNIGSGMCKIAGFAGDDAPRA VFPSIVGRPRHQGVMMVGMGQK DSYVGDEAQSKRGILTLKYPIE HGIVTNWDDMEKIWHHTFYNE LRVAPEEHPVLLTEAPLDPRA T REKMTQIMFETFNTPAMYVAIQ AVLSLYASG/RVTTGIVMDSG DGVTHTVPIYEGYALPHAILR LDLAGRDLTDYLMKILTERGYS FTTTAEREIVRDIKEKLCYVAL DFEQEMATAASSSSLEKSYQLP DGQVITIGNERFRCPALFQPSF LGMESCGIHETTFNSIMKCDVD IRKDLYANTVLSGGTNMYPGI ADRMQKEITALAPSTMKIKIIAP PERKYSVWIGGSILASLSTFQQ MWISKQEYDESGPSIVHRKCF
26863	57231	A	27016	2	438	ADLLQVSNVCVSSCQPPAFLVL FSSSRLPAGEGRGRPGQTQRPSS LEGAWHSVTLERRCLVSHLINL REAGMYPSPRCHHLPDQLV*T EGGF*RPRLGWQRCHGTQPPQA PSQPAFRSKHPRKGMPALQQQP GSGLCRPLPCRCR
26864	57232	A	27017	112	493	AHSRTPARPENRAAASAPRKPR RAMSSPPEGKLETKAGHPPAVK AGGMRIYQKHPTGDTKEEKD KDDQEWESPPKPTVFISGV I ARGDKDFRPADAQVAHQKPHA SMDKHPSPRTQHIHQPRK
26865	57233	A	27018	1	1176	
26866	57234	A	27019	3	307	
26867	57235	A	27020	86	179	SVKRRK*SLLTWIGMRLQRQHR ECLAQVGS
26868	57236	A	27021	1	948	
26869	57237	A	27022	3	534	EGAHFRAAHHPRSTGSRCPGSL QPSRPLVANWLQSLPEMPVDF T GYWKMLVNENFEYLRALDV NVALRKI/APTLCLKPDKEIVQDG DHMIIRLTSTFRKLTWNFIQVG KEFEEDLTGIDDRKVHDKQ*A WDGDKL/QCVQKGEKEGRGW TQWIEGDELHLEMRVEGLVC KQVFVKVQ
26870	57238	A	27026	1	2400	
26871	57239	A	27027	294	425	
26872	57240	A	27028	1	797	
26873	57241	A	27029	1	173	
26874	57242	A	27030	1	1047	

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26875	57243	A	27031	2	1019	PTSAPIHLSLSPRAVIERRSRALDW NASPSLSDPQGLDASLPFPPSHKR SRTASPEPAEHPVMDKNE/LVH KAKLAE/QAERYDDMAACMK VTEQGAELSNEERNLLSVAYK N/VVGARRSSWVVS/SIEQK/T EGA/EKKQQMAR/EYREEIETEL R/D/CNDVLSLVGKSSLIPNAFT SRRSKVF/YILENGKGDYLPFTL GWRVAAGWMDQERGLDFPVH NKAYPRKAFWKSAAKGNNGPT HPURLGLVALNFSVFYYEILNSP EKACSLAKTAFDEAIAELDTLS EESYKSTLIMQLLRDNFDIVG HRDTQGRKKLEGREGGENL TGPFPTFCSWPHS
26876	57244	A	27032	177	477	
26877	57245	A	27033	1	1290	
26878	57246	B	27034	49	1112	
26879	57247	A	27035	98	245	
26880	57248	A	27036	1	351	
26881	57249	A	27037	3	471	
26882	57250	A	27038	1	440	MKMRVGCMLTAESLSDGGNS HQRTL.SLFESKESQCEARGEV SKAGVWLVPLEPSDALPKITS LVRPAVWPSPSEAGLCEVRGG VLGKASKAPIKEPQLDRGMGL GAQRRGSSGTEVQSGETLGASG SPRGLLEPRPDWVSNNGAGSLG FQQLPIVDKIRTIAQAVCGAKDI ELCPEAQVKIDRYTQQYYSC*N PKLPAPLFTQSGLSGSKSPLGLP LAPRVSPDCTSVP/GAP/SAAGP RAPCPDPAVAPLWGLCWFPPEL
26883	57251	A	27039	1	1113	MHQEDLRAWYLDLGLPSHQ AQPTAWKCQRAPSPYTHQDMA LIPSPARWLSPEKEPKQGEVG EKSLPDPDTLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRLLADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIIJLCTLVNKLQPGSV KINASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANLFESE NNMQVRVSLALAGAKTKGL RSGVDIRDKYSEKQNFDDTTM KASQCVIRLQITNKCASQSGMT AYGTRRHLYDPKNRILPPMDNS TISLQMGNTKNCASQVGMTAPG TQRHIYDTKLGLDKCENSSMSL

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26884	57252	A	27040	347	1061	
26885	57253	A	27041	212	386	LQGSWVTSGLERICGSILGTIPL AHEVTDTDQHGRMVYQVATAG F*SSLGAASIGTQGL
26886	57254	A	27042	1	1017	MHSRRERARGRLGAHHPLVDN GPPQSLRAPPLSPLKTAGAKSI WEPLASARRPETPERTLQKTP EQVPTNFMGALHMKTSAPLSS RNGEGRRGTSVASCSPVWVGA VCSAERQPTQRVREALMGGW RAGAQNRAEDQVDEFTEVGF RRWVIKNYDELKEHVLTCCKE VKNLDKSIHPEISRLHEFITTTHT LPVIGGKVSLLSKCQDNAEQKQ SQGCSQEGHEVYDPRLNSSSS SSSGGGQSPGLRRCSTSAAAAA ALEGAALKPMPVHAGLVGSGE GGGAGAVAGPCSRWGATTA ASSAQAQPVRRGSSGAQGH GRRRRQAGKGGPAG*TA AP*GRGAEPGAAALLNLGGSG GAG*SAALKPMPVHAGLVGSG EGGGAGAVAGPCSRWGATTA AASSAQAQPVRRGSSGAQGH RGGRRRQAGKGGPAGSS
26887	57255	A	27043	644	949	
26888	57256	A	27044	811	1886	
26889	57257	A	27045	1	410	HAHSLNSIILPTLEIHKV*IQIY A*GCKRISNNCWCHQHLLSIS PDLRINGEKECGSPWIGVEAR/ MGGELSSAVGLTSLLLYQQVPF HPHFQSPFTIPRESILLQHASCW RQHHLHTGIYSSYLPGWKQFES
26890	57258	A	27047	1	2445	
26891	57259	A	27048	1	457	
26892	57260	A	27049	1	873	
26893	57261	A	27050	2549	2728	ATSRSSALITSSKYPGKF*LILI* RSTLETANSISARLNNPFLRKYP SYFSLFMGTTRI
26894	57262	A	27051	277	394	
26895	57263	A	27052	2	1394	
26896	57264	A	27053	1	1091	
26897	57265	A	27054	1	1404	
26898	57266	A	27055	2457	2674	ANHCYLLSELQHWSDCPVVLQ SAG*RH*DRN*DGNY*SR/SL *SR*STTK*RNTPCSQVSSLSRLS TRSA

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26899	57267	A	27056	716	1455	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGNYS TGDNHTLR/DPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQS AKKRDAELANGA LGHIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGK WYLF TDSRGSKMTIDGINSNDIYMLG YVNSLTGPYKPLNKTGLVLQ MVLIPNDVTFYSHFAVPQAK GNNVGIHQATLTNRGFFEIKKA TFAPSL
26900	57268	A	27057	66	197	
26901	57269	A	27058	379	905	AGNFVHITVRKMLWIRRDQQQ S/DKQDIQTAHRSYSVLKGYND MYYGWPCKKVNEISGQLASEP A*SLVLPAAQ*QAPASGSPWLS GGPQQVEDAGAGYGFAPGQPP PPPTQPRSACSRRAAGSQFHG RPLLPRQA AKARAPSLGCGSL GRFSTGVRPDKCIPPETENAA
26902	57270	A	27059	1	1608	
26903	57271	B	27060	1	1974	
26904	57272	A	27061	2712	3216	KTGRGPTDKFGVANDPILKDQT QEWSSGAPFISDGKFRIFYTD YSGKHYGKQSLTTAQNQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENG YQGE ESLFNKAYYGGGTPFFRKESQK LQQS AKKRDAELANGALGHIEL NNDYTLKKVMKPLITSNT
26905	57273	A	27062	1	3066	
26906	57274	A	27063	1	972	
26907	57275	A	27064	14	273	
26908	57276	A	27065	42	302	
26909	57277	A	27066	1	487	MGLSLKGPESAPIKTPQFNKIL FKPIAVYNRTQFRLSETEKTN PYAMRLYESLCQYQRYQLPQS YQRISLTSAAASCRSVLMRSTA ELQCASHTLRKRKAARRLSLS EMPRKQGDYRTRIWKFEDGLS NVLVIQLNKLIIICVMCLVRDCD VLKTYFHR
26910	57278	B	27067	1	1035	
26911	57279	A	27068	132	230	CHYFACMWSGCEVYS*SAPG** C*EDLSGMVR
26912	57280	A	27069	1	2784	
26913	57281	A	27070	855	980	LSCSGWRAG**ADGCIHQIG*RL SPNKCL*TWSALCKPIAE
26914	57282	B	27071	85	863	
26915	57283	A	27072	345	500	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
26916	57284	B	27073	1	1116	
26917	57285	A	27074	1	1173	
26918	57286	A	27075	1	999	
26919	57287	A	27076	771	908	
26920	57288	A	27077	104	547	LFPRLLSCLTTPHCSFSICFVIC SRTLILKGSSLMYVFCPLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLFKFLKNGLNFLHSHVGTTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDADDVLSTEVKRVITS SASNITPAFFCS
26921	57289	A	27078	34	1353	
26922	57290	A	27079	213	338	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWSALCKPIAE
26923	57291	A	27080	1	1246	MVKVGTSTYVPINVSFSKVGPG LPGINRDRITRIYLFCEVIFRHRKD RESADLGSDGQNGRPWIGEA VAAAAADGVTFSVPVTPHTFR HSYAMHMLYAGIPLKVQLSLM GHKSISSTEVYTKVFALDVAAR HRNRFTQFRLSETKEITNPYAM RLYESLCQYRKPDGSCIVSLKID WIHERYQLPQSYQLYFYELAIPV GYFYPGSFSTASRILLHPRGLR AITIAVFGKQNTYIRLEPKINV LEQITKHIEKLQCGGVVKLSR RGNNQHISSTYDINRADYPG*A RDPHMLRLRLAIETVAHDYDVIV IDSAPNLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVLDLKGFEPPDRILLTKYSN SNGSQSPWMEEQNSGCRGKTS RVEVPHRDSQFKVIKLVTLRQL VTLYDPVDFQRDDA
26924	57292	B	27081	1	1041	
26925	57293	A	27082	1	1011	
26926	57294	A	27083	2	1007	
26927	57295	A	27084	1	738	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
26928	57296	A	27085	1	1439	MAETA VINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYL FV DQIRKSDGTLQEHGDCIHHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPRGLYSVHIN PYLIPFFIGLQNRFTQRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIER YQLPQSYQRV WTPGINCPGCPGVWTPGINCP GAWGIHGPHGSAENTGPHLPG QTSAQLETSLPSLRSAELELA QLSPRRKQNRSLQNIGVTPSLR VPWPKASNVQQFIDEENYTS DNHTLRDPHYVEDKGHKYLVF EANTGTENG YQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGHELNNDYTLK KVMKPLITSNTVTDEIERANVF KMNGKWYLFDTDSRGSKMTIDV PQAKSNNVGITSYMTNRSFFED/ KKATFAPGLWNIAIKTS
26929	57297	A	27086	345	563	
26930	57298	A	27087	1	1188	
26931	57299	B	27088	1	1186	
26932	57300	B	27089	1	1090	
26933	57301	A	27090	183	410	
26934	57302	A	27091	1	1557	
26935	57303	A	27092	888	1165	CTRERRIKARGPPAGKRWLLLS GSSGRKHHL*QDPRPGSQTAGD LPEPAR/PIIVIGESQMGLEDCQ FQFRNGRWNCALGERTVFGK ELKV
26936	57304	B	27093	1	1027	
26937	57305	B	27094	1	1117	
26938	57306	B	27095	1	1377	
26939	57307	B	27096	1	1014	
26940	57308	A	27097	1040	1285	
26941	57309	A	27098	901	2277	
26942	57310	A	27099	1	1122	
26943	57311	A	27100	1	1137	
26944	57312	A	27101	1	1881	
26945	57313	B	27102	1	1211	
26946	57314	A	27103	294	506	NRRPGSAATVWAAAAEPSE NNPALENR*SSGFSWGFFSGYQ RCRESRATTAPGYGNSRTG*AT CWLYN
26947	57315	B	27104	1	1073	
26948	57316	A	27105	1	1809	

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26949	57317	A	27106	1688	2187	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVA\RKDRES ADLGSDGQNGQDLDWGGVAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS INSTEYTKVFALDVAARHRV QFAMPESDAVAMLSF
26950	57318	A	27107	782	1402	LFPRLLSCLTTPPHCSFSCFVIC SRTLILKGSSLIKLLFYKIPSMVL SSVLLLEVKSHIVGPGLPGINRD TRIYLFCEVIFRHRYLFAISSWS GVTVA\RKDRESADLGSDGQN GQDLDWGGGAAAAADGVTF VPVTPHTFRHSYAMHMLYAGI PLKVLQSLMGHKSISSTEYTK VFALDVAARHRVQFAMPESDA VAMLKQLS
26951	57319	A	27108	197	421	LAMPGAGFSSSLRMASIFSIHVS GTRDLSRVSTILSPLYNTVAPG AN*CRELKLVLDDADDVLSTEVI RVITSSA
26952	57320	B	27109	1	934	

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26953	57321	A	27110	1	2047	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQVRVGTIEQI NHMRDVFGRRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWVVDLHHIAEDTLLPF YLGEKDDVYAIKPTCWPGLDI IPSCALHRIETELMGKFDGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKTVDLKGFPDVRILLTKYS NSNGSQSPWMEEQIRDAWGS VLKNVVRETDEVGKGQIRMRT VFEQAIDQRSSTDTSSTPAAP MVDLSLIARVGVGMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQTPAFGRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSPGELSARSGDALQ KAFTDKEELLKQASNLHEQK KAGVIFEAEVITLLTSVLKTS ASRTSLSSRHQFAPGATVLYKG DKMALNLDERSVPAYIIRS CGRKGFASAGVGGCROWLNY AASEQVLRVHHMRCEIPIRCV
26954	57322	A	27111	1175	1298	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWASALCKPIAE
26955	57323	B	27112	1	1056	
26956	57324	A	27113	1979	2217	WLSVRVDGGANSGLKGHGSK KCCT*NG*SW*RSDFENCF*T EQ*STLFNGAWRNALSIWEPV CN/GNFRSSD*TTLGD
26957	57325	B	27114	320	1633	
26958	57326	A	27115	606	705	
26959	57327	B	27116	1	4118	
26960	57328	A	27117	4048	4051	
26961	57329	A	27118	1791	1884	ADGCIQIG*RLSPNKCL*TWAS LCKPIAE
26962	57330	B	27119	1	2436	
26963	57331	A	27120	1	2449	
26964	57332	B	27121	173	4112	

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26965	57333	A	27122	916	1568	HHSHEQQFQWPVGASGVDRW AGYLHQFRSLTQFQYGAEPDR KE* CQIFIMQKTL SCL SILGR TMSLMQ
26966	57334	A	27123	1268	1773	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVAIRKDRES ADLGSDGQNGQDLWDGGGIAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEVTYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
26967	57335	A	27124	606	852	HQILFDRTPVSDQSVKEKKG*D HSVRPQ*AAPGHVHYLTIPEKS SQHYHPRTTSE*TSGRYESSGG LSFSQCMRGALEFCC
26968	57336	A	27125	1	2680	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGLTRRAEDVFPPIV GVAAIKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWWPDLHIAEDTLPLF YLGKDDVTYAIKPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPAETSQGAL GTLANVVTSLANLSESLNNGDT SEIQPEDQSASEITRAFDTLAKA LNTTSSSSPSLADGIDTSGGGS IHVISRDQSTPIEVEGPLLSDTH VTFKSIREDRNGRSQKTVHTEG DMNMNIKKIVKQATVLTFTTA LLAGGATQAFKENNQKAYKE TYGVSHITRHDMLQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTVAEYNGY HVVFALAGSPKDADDTSIYMF YQKVGDNISIDSWKNAGR VFKD SDKFDANDPILKDQQTQEWGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQNVSVKSDDTL KINGV EDHKTFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYL VFEANTGTENGYQGEE
26969	57337	A	27126	2014	2138	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWSALCNPTAE
26970	57338	B	27127	1	7616	

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26971	57339	A	27128	240	719	HSKKLVTLSHGSVMAETAVIN HKRRKNSPRIVQSNLDEAAAYS LSRDQKRMVLYFVDQIRKSDGT LPEHDGFCYIHVAQSAEITGLTS VGNPVRIYGRH*RVSRGRKVV YRPEEDAGDEKGYESFPVVIK AHRPSRGLFSGHIPPIHSLLYR
26972	57340	A	27129	1505	3812	
26973	57341	A	27130	471	566	
26974	57342	A	27131	1	229	
26975	57343	A	27132	121	303	
26976	57344	A	27133	183	524	MSTPRPFVPAFVGRPPSLLFVP AARLTDVRGRKVRACGLSPR LRSPSSSSATRVARHSIGRPRVA RLSTVFVAVCVESPSRQRWCL FALAATPRAPGTLA*SCLTDSFS A
26977	57345	A	27134	1	1025	MIFVLQIRVRGHDDSLKNHLV FLVIYGTNGTFNQTLVTDNGL APFTLETSGWNGTDVLEKGFQ MEDLVYNPEQVPRYYQNAYLH LRPFYSTTRSLGIHRLNGLPKC GQPQEVLDVYIDPADASPDQE ISFSYYLIGKSLVMEGQKHLN SKKKGLKASFSLSLTFTSRLAPD PSLVIYAIFFSGGVVADKIQFSV EMCFDNGQDLDLTSTVRVTRSSA SVMVYGAASEAIGQRQSSAAKP RRSQSDSLGPEFQGLWERLPGL RINGELITAYPQVVVVRVPTPW VQSDSDITVLRHLEKMGCLM NRPQAILNCVNKFVTFQELAG HGVPLPDTFSYGGHENFAKMD EAEVLEFPMVVKNTGRHGRMY ELLVSTMGCNSGMVTTPIKWL SMISVQCLANGTFLSPSLTKCPK GIRASVPLSGGPRSLKARTFSAF SGPVRSDQEALPEAYEPIEV NEFGEDLLAMVEDEILALPVV PVHDSEHCEVSEADMVFGELPE EAQKPNPFAVLASLKRVRMSA VQKNKPTRSKRGMRSHDALT AVTSLSDKTSGEKHLRHH*SA DLAAAPRAPGTLAQGLTDSFS
26978	57346	A	27135	79	306	SGDLPEINPLSSCSLLREKDP MTSGPQTNPQKHLINFKSGPH WKSDCSTHLAATPKAPGTLAQ GSLTDSFSA
26979	57347	A	27136	159	254	
26980	57348	C	27137	63	370	
26981	57349	C	27138	107	408	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 9/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
26982	57350	A	27139	210	291	
26983	57351	A	27140	395	680	
26984	57352	A	27141	157	485	
26985	57353	A	27142	1	507	
26986	57354	A	27143	1	1041	
26987	57355	A	27144	1	671	GASGAAAYGADMAKSKNHTT HNQSRKWHNRNGIKKPRSQRYE SLKGVDPKFLRNMRFACKHNK KGLKKMQANNAKMSARAEA IKALVKPEVKPKIPKGVSRKL DRLAYIAHPKLGKRARARIAKG LRLCRPKAKAKDQTKAQAAAP PSVPAQAPKDDTSNIFISNRKR GCDFTKKETNIPKVLITSMAPSL MSLYSVTRNQTTKPPSRHKNL KQGLEPLY
26988	57356	A	27145	6	448	
26989	57357	A	27146	930	1307	
26990	57358	A	27147	1	675	
26991	57359	A	27148	142	456	
26992	57360	A	27149	3	175	
26993	57361	C	27150	378	434	
26994	57362	A	27151	1	792	
26995	57363	A	27152	1	578	MVRCVRLVEAGSVVRYLSTSI RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAVVRARELHTLEV/TGLET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRILGASL/HTSASKHTM VRALTYCSSREFTTAI
26996	57364	A	27153	1239	1905	SAAAPATGVPACRAGAWVSA APPAEGRPARARRHPGRCLEAA GPRGQRGAHGH*ARAGSPQP GAPPCHPGLIPARQPLGLPRRTR CFGIAQRGRAARHCLLSRPSA KAKRNSSYREPGMGWSPQA LGEYKGQSQAQSARLSGAASQ GRRARHLRGKAPAWNPPPPSP PPPALGLPLRTQREATRKPRRE EARRPRPRPLRPGGANGSPGPP RAARA
26997	57365	A	27154	1	1275	
26998	57366	A	27155	3	92	EAVDPHSECYSS*RWCVRSFFIL VGLWSH
26999	57367	A	27156	2	367	
27000	57368	A	27157	98	293	GQTFATASISLLRYATGCGVFP RV*IRSPRAIPALSGDWAPFVS LSEPRFVCLRAMTKAAAF
27001	57369	A	27158	3	211	

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27002	57370	A	27159	1	519	GQLI/LKDTFITQSAADIRKQFQ KQALGPEHNLEALLNLAILVFFY NRDQEEQAQKEKRDQRKAAPL IMALRQTLVVQRGQKMEQANH LIPGYSEIARPLYTLIKEIQRANT HQVEWEPEAETAFAKPLKQALV QAPALSLPTGQNFSLYITERAGI ALGVLQTHTGTPQLVAAYL
27003	57371	A	27160	72	381	DSHTRSGITRWGIRCSRSGSSPSR RARWGRWGGLAAVALRRPAP AAGGTAPRGCLPAA*GSPAPP SGS*SGSSDRPARMPLVVGLSH EFE*GLAGVDGEVLPPSRCVAL LLLRVERLHVAVYLPREALHQL IPLALDLDLLIARLVCHWLWG CPTLSKDKSYSCSLCDV
27004	57372	A	27161	515	747	SHGNSGNFQGTDRDITSL* AQLT TSTKDPWTDPPALWPRVFPSSGG HYNCRAPSSPTIQQEVARAVIT QFPTAAGVSCL
27005	57373	A	27162	1	663	
27006	57374	A	27163	1	1980	
27007	57375	A	27164	1	672	
27008	57376	A	27165	1	691	
27009	57377	C	27166	1	1491	
27010	57378	A	27167	830	2592	
27011	57379	A	27168	1	3744	
27012	57380	A	27175	2	365	QWDWAPWSRGWCSSGRLGPH RSPRSGGSGRRAAGPKPCPSP RSDAPAQPRGRSRRVLPPLQVQ AEPPEPWVPLPAAPKPLARPEA GMAGPGGRRTTSLPRRRGCCG CCPASSCFSSLSC
27013	57381	B	27176	1	1392	
27014	57382	A	27177	79	1241	
27015	57383	A	27178	3	299	

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27016	57384	A	27179	1	812	MPTVLACPAFDSRGSPICRFDPPELTSQVRALEESPNAILPVCGRDVKFTLEVLRGDSVEKTSRVVSGNERDQELLTEDALDDLPSFLTGGQTPAFGRRVSGVIEIADGSRRRKAAALTESDYRVLVGELDDEQMAALSRLGNDYRPTSAYERGQRYASRLQNEFAGNISALADAENISRKIITRCINTAKLPKSVVALFSPHGGELARSQGDALQKAFDTKEELLKQQASNLHEQKKAGKRSRRLHHTLLRVVAEIDKPDPRDELAGLLQFAGGPLQTLFAWVSPVEAAEQQRLLAPSSGSFIP EG*DHPVRPQ*AAPGHVHYLTI PERSSQHYHPGALQE
27017	57385	A	27180	306	701	
27018	57386	A	27181	1	396	
27019	57387	A	27182	1	1263	
27020	57388	A	27183	1	873	
27021	57389	A	27184	149	421	
27022	57390	B	27185	23	268	
27023	57391	A	27186	1	363	
27024	57392	A	27187	2	398	TKFAARRPALAACAAISKIKARDLRGKKKEELKQLDDLKVELSGLRVAKV/TQGGGAASKLSKIRVVRKSIARVLTVINQTSKKKT FREILTRGKKYKPLGPCGP*GRT RAMRRRRFKPSTEGEP*RTQGSR
27025	57393	A	27188	224	547	
27026	57394	A	27189	1	888	
27027	57395	A	27190	280	1170	
27028	57396	A	27191	1	191	
27029	57397	A	27192	438	1240	
27030	57398	A	27193	168	378	
27031	57399	A	27194	1	1362	
27032	57400	A	27195	2	918	
27033	57401	A	27196	38	397	RRCRPTMPRPWCTCRGYQGPRKAQGG*AQDPKGCQPQARSTCLHCPQAW/RVLVPVLPVPRSGCAGQ/MAKAKAKAKDQTKAQAAAPASVPAQAPKRTQAPTKASE*ISLPT*GQKDWDGP
27034	57402	A	27197	1	1206	
27035	57403	A	27198	734	913	
27036	57404	A	27199	3	778	
27037	57405	C	27200	164	274	
27038	57406	A	27201	1	2700	
27039	57407	A	27202	1	747	
27040	57408	A	27203	164	409	
27041	57409	A	27204	152	380	

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27042	57410	A	27205	230	2579	
27043	57411	A	27206	1	2433	
27044	57412	A	27207	1	528	NHQRNDFTISPGVKADSRSTSPI PQQPASSFDITEAAVSFAKDSLA GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP/ TQALNFTFKDKYKQIFLDGVVDK RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVKG AGAERELRGFGDCLVKIYKSDG IK
27045	57413	A	27208	1	292	MTSKDKTSRGTIRQQHSRFFKI RCSAATTAGTQANRVWSGPLA NSNRPAAEAGVSTAAAPDGGPPP PSVPTVDSDSLESAQFKCDNLK TCHTSHGSVMAETA VINHKKR KNSPRIVQSNDLTEAAYLSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDEKGYESFPWFIKRAHSP SRGLYSVHINPYLIPFFIGL*PDK EGNEIWVDMYTVKPSGWTVRT FDKPRKRFIAFFIAGILFRAIKNH FLPRETLQCLPYILTGFRRGQSE YFSIFSNMDLADTVMFL
27046	57414	A	27209	1	1452	
27047	57415	B	27210	53	844	
27048	57416	A	27211	281	624	ACSDVWSKFRLRWSPNRCQE RPSAEKMSPHPPSAARHQASWS ARRLTQWPRPCHTQ*GQSEEH GHRSGMLMPAGVTHQLPDEHAIT PHLQSTAPIPEPKTSLSHKDSSLQ GTGK
27049	57417	A	27212	3	411	
27050	57418	A	27213	265	480	LDLTILTASDGRPTYTP*FLLS/ CFCYGFFCYIFGCSCLARAR AGGGGVPAAHRAAGGRSRAPE RIPPH
27051	57419	A	27214	294	620	
27052	57420	A	27215	1	420	
27053	57421	A	27216	1	342	
27054	57422	A	27217	175	244	DLLEMGSFFVQCRTAIL*RKQN
27055	57423	A	27218	11	951	

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27056	57424	A	27219	20	1654	ELRFPAACSQLQFSDGLHRVDQ PPSSMCVSAADLWLCEAGKLL VVPMDGSHWFTMRSVVEKLIL RGHEVVVMPEVSWQLGRSLN CTVKTYSTSYLTEDLDREFKAF AHAQWKAQVRSLSFLSSSNG FFNLFFSHCRSLFNDRKLVEYL KESSFDAVFLDPFDACALIVAK YFSLPSVVFARGIGCHYLEEGA QCPAPLSYVPRILLGFSAMTF KERVRNHIMHLEELFCQYFSK NALEIASEILQTPVAYDLYSHT SIWLLRTDFVLDYKPKVMPNMI FIGGINCHQGKPLPMEFEAYINA SGEHGIVVFLGSMVSEIPEKKA MAIADALGKIPQTVLWRYTGT RPSNLANNLTILVKWLQNDLLG HPMTRAFITHAGSHGVYESICN GVPMMVMPLFGDQMDNAKR METKGAGVTNLNLEMTSEDL NALKAVINDKSYKENIMRLSSL HKDRPVEPLDLAVFVVEFVMR HKGAPHLRPAADHDLTWYQYHS LDVIGFLAVVLTVAFITFKCCA YGYRCKLGKGRVKKAHKSK
27057	57425	A	27220	1	2022	
27058	57426	A	27221	124	205	
27059	57427	A	27222	248	443	
27060	57428	A	27223	263	415	
27061	57429	C	27224	1	717	
27062	57430	A	27225	349	1125	
27063	57431	A	27226	629	796	
27064	57432	B	27227	1	388	
27065	57433	A	27228	2	346	
27066	57434	A	27229	448	555	
27067	57435	A	27230	2	423	CEPIKVYVVGNGAVGKTCLLI SYTTNAFGEYIPVTFDNYAN VMVDGKPVNLGLWDTAGQED YDRLRPLSYPTDVFLICFSLVS PASFENV/LCKGAVKYLECSAL TQRGLKTVFDEAIRAVLCPPPV KKRRKRCLLL
27068	57436	A	27231	1	1503	
27069	57437	A	27232	1	635	

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27070	57438	A	27233	3	1107	AVFLSFGWWPLPGIGFQSAEGE AAWTAAPAPSAPPPSKPRARPP RPEPAASYLSALPPPPRPSERPS MQAIKCVVVGDAVGKTCLL ISYTTQCHFLGEYIPTVFDNIYS A\NVVMVDGKTGEIWLWDTAG QEDYDRLRLPLSYPANRMC*S I CFSLVSPA/SFENV/LVQKWYPE VRHHCPNTPNPVGTKLDLRD DKRHDSRNLEKKLT/PITYPA GS*AMAK/ERLGAVKYL/CAP AAHTSEGLKTVFDEAIRA/VLCP PPVKERGRENCLPVVNVSA PSF LGSCPLGTFCLCSKKNKKKKQ KKKNNGGAFALNANFLLQINFS IKPFFEPISNFKVLVFLNVRVQT HILLKFSPKMTSLLKALFFK
27071	57439	A	27234	3	203	
27072	57440	A	27235	1	112	LGNTWG*QPCRLKIWLSLEFT KINVIRHMKFKRL
27073	57441	A	27236	1	513	QHWGRLKRAFEQWQVPRFG HMPDPGPVKPLQPVETVRGN DYKFLLFHFWDEWLKYFSADE FFIPGKLCAIVF*KRL*RP GAVA YACNPSTLGSGRGWIT*GQ EFE TSLTNKEVKVLSIDQRNFKLRSI GWGEEFSLSKHPQGTEVKAITY SAMQVYNEENPEVFVIIDI
27074	57442	B	27237	125	302	
27075	57443	A	27238	93	432	
27076	57444	A	27239	3	279	
27077	57445	A	27240	263	446	
27078	57446	A	27241	237	369	
27079	57447	A	27242	389	836	
27080	57448	A	27243	1422	1580	
27081	57449	A	27244	103	444	RSLTCPGDMFPVVLVINIQLLT YANFCSWLES�PRKWDFLFYCI VRLQIFQTFMLCFLNLTPLRNF FYQIP*HSLKFKVPQISKAEAKC HQSCLCIGRVTFIPVPNKFFISI
27082	57450	A	27245	3	242	MHRNAQHVVKTAKPWGLHPL KPQPK*YSGPF*PPELQRCCKAT GP*GCTQQGGPGPGQNNFSL LGLQACDGRDCHEGL
27083	57451	A	27246	506	664	
27084	57452	A	27247	1	1515	
27085	57453	A	27248	269	541	RFPNLNS*LLYTRGLTPHESQ GLGLAPSEAMAQTIPWPLATA RLAVTGNQILMQISAAGLNFS S ENGAFISIALSGCKFFKLLCSAS
27086	57454	A	27249	1	564	

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27087	57455	A	27250	2	235	
27088	57456	A	27251	3	1393	
27089	57457	A	27252	28	271	
27090	57458	A	27253	12	485	RMAFCRASQADQDRFCIYPAY LNNKKTIAEGRRIPIKSAVENPT ATEIQDVCSAVGLNVILRKIKM YF*EWNRDVQYR/GRVRVQLK QEDGSLCLVQFPS/RLYTKPNF WFLGKSVMLYAAEMIPKLKTR TQKTGGADQVFQQGECS*GKG GKQKEVT
27091	57459	A	27254	1689	2176	APPGMGAASLCAFGLLVTFAT ASPRYAMVQPSFRLGTLGQA EADPEFVSSGVSPPSFLSPLPA APGARRG*LQRGDLGRQAPPPA PGCAPGLA*GRPPAPHL*RLCSR PTFFPPPPANSSRLALADSPPRQ LQGARPP*PVPGRLLTSTGTPRPL PRPLGP
27092	57460	A	27255	263	439	
27093	57461	A	27256	1	499	MSELPTIATKRIKHLGIQLTRD VKDLFKKNYKPLFNEIKDDTNK WKNIPCLWIGRINILKMAILPKV IYRFNAIPIKLLMTFFTEMENTT FKFMWNQKR/CPHCQDNPKPK EQSWRHAT*LQTLQGYSNQN SMG/TWMKLETILSKLSQGGK TKHRMFLIGGN
27094	57462	A	27257	1940	2062	
27095	57463	A	27258	1232	1432	
27096	57464	A	27259	168	1189	
27097	57465	A	27260	1	1760	
27098	57466	A	27261	453	543	
27099	57467	A	27262	873	962	
27100	57468	A	27263	8	411	FSRCRCSGR/YLCMASCL/CFHH CWWMAASHHWPI*RTQV*CAC WEGRHLG/CAPKCLSLGFTRL LACVLLWPLQSVIPIHIQVSITV RVLFAAAHDEARASEATFQESG GPYPLLSTPLILLKAVVVLMLD AHAS
27101	57469	A	27264	1	552	
27102	57470	A	27265	828	1211	
27103	57471	A	27266	428	655	DQKVPPLEMYFGIEVKSLLKQLR SISA*SLFSSRALKEDSGLLKLK QPRSSGVIPRRFIVSWPWKMVR QPVLFSVG
27104	57472	A	27267	1	855	
27105	57473	A	27268	1	1261	
27106	57474	A	27269	164	260	

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27107	57475	A	27270	147	224	RLTLDPHLGSLLDHHRVALGNS YSGG
27108	57476	A	27271	1	837	
27109	57477	B	27272	184	288	
27110	57478	A	27273	1	286	
27111	57479	A	27274	1	699	
27112	57480	A	27275	1	3660	MTGICYTEDERSYKKNQAQPTA ASKKQKETQKFCRLVDDGQKQV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQQA WPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAAQRAQSLPEPYGTG LRALAMPGRPESPVPFRSQEVV ETMCPVPAATSNVHMKKISI TERSCDGAEMKWEDQNIQD
27113	57481	A	27276	1059	1229	
27114	57482	A	27277	2	4735	
27115	57483	A	27278	415	825	SCADFQDYWDQREYTYNRPH ASRRIVLDFLLFPEW/PTFVAFW APLFNPSKRASLYRFLSCISSLSF GSHWGSVPGNWLVTYSWG/SL VISRCMFL*PLSCCLEHSPPFICV KEEHEQLVAISPSGVMLDNLSEQIN
27116	57484	A	27279	1	1326	
27117	57485	A	27280	2976	3068	VWTLALNRLGQQVSIQCG*PGTE DSKGDWLL
27118	57486	A	27281	78	220	APTSLHS*SYFKNCGHRLRWV ITHIRLVISWATYLVQNNIQLR LF
27119	57487	A	27282	1	1077	
27120	57488	A	27283	307	922	QVVPSSLSAISQSPAPCG/CSP*G PSPGAT
27121	57489	A	27284	1	4560	
27122	57490	A	27285	87	237	LLFFQLGGDAFSKFKSSGVNFR NSLICQAWGKRVFSALLCHLSE YTSPL
27123	57491	A	27286	1	246	
27124	57492	A	27287	46	396	
27125	57493	A	27288	1	552	
27126	57494	A	27289	3	418	AEKCPCLGAFGFGWDHPRRPG SWGAWSEGGSPPARIVKMMLR KQTPSDFLKQIIGRPVVVKLNS GVDYARGVLACLADGMNIALE QTEEYVNGQLKNKYGDADFIR GNNVLVYSTQKRPDVRTPKRA TLFIVGYIFL
27127	57495	A	27290	202	450	

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27128	57496	A	27291	304	642	
27129	57497	A	27292	75	393	
27130	57498	A	27293	1	678	VFGLGSVAHMLLNKTFGSYLGVNLGFGFGVTMGVHMAGRSGAHMNAAVSLTNCALGRVPWRKFPVYVLGQFLGSFLAAATIYSLFYTAILHFGSGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEAWLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWGKQVFRVWHLLPLGLHWLHHPITGAPEIGGFCGV
27131	57499	A	27294	2	1694	
27132	57500	A	27295	1	356	GIFVTYLPDHMTLWRGFLNEAWLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWGKQVFRYFPCPGPIPLSFSVGPCLVEGWGVM
27133	57501	A	27296	1	544	
27134	57502	A	27297	320	610	LREYTIINHTAHMPMEWASKKRAPRALKEIRKFAMKEMGTPDVRI DTRLNKA V WAKGIRNVPIRIRVRLSRKRNEDEDSPNKLYTLV TYVPVYHFQK
27135	57503	A	27298	1	303	
27136	57504	A	27299	1	1311	
27137	57505	A	27300	1	3126	
27138	57506	A	27301	2	779	NRVLLAMVNPTVFDDIAVDGEP LGRVSEFVRGLDTKK*LLI*SIK LC*QIG/LFADKGPRGTA*FSL* ATGEKGFL*GVPCFHRJPGFM ICQG/GDFTRHNGTGKSHLW GRNLKDENFILKHTGPGILSHG KMLDPNTNGSQFFICTA/KTEW LDGKHVVFGKVKERHEILWEA MGALLGPRNGKTQEESEPIVPG GQLRIKFDLVFYSLTTHIIFPCSF KESTPPPHLLASILESLCSRLQFP FGFHVFLVPCHA
27139	57507	A	27302	143	390	
27140	57508	A	27303	249	1516	

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27141	57509	A	27304	2	645	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDITKK*LLI*SIK LC*QIGLFAADKGRGTA*FSCGL* SIEEKGFGL*GVPCFHRIPGFM/ CQG/GDFTRHNGT/GGKSHPM GKKFE/DENFILKHTG/PGLLSH GKCLDPNTNGSOFFICTA/KTEV VGMAKHVVFVQK*KKGMKYC GRPWFRFG/SRNGKTQQRKITI C*LVGQLRNKVLTWVF
27142	57510	A	27305	72	387	VCLQHGPWSSLKHVQGWRRD CHGLSLGPRTHVQAGTLPKPTL WAEPGSVITQGS/VTLWCQGI LQTQEYRLYREKKTAPWITRIP QEIVKKGHDPISITWEHTG
27143	57511	A	27306	1	322	
27144	57512	A	27307	1	1125	
27145	57513	A	27308	1	1419	
27146	57514	A	27309	198	1634	
27147	57515	A	27310	78	216	
27148	57516	A	27311	1	489	
27149	57517	A	27312	18	463	AEGVEPGSPRVVLESEQFLTE LTRLFQKCRSTSGSVYITLKKYD GRTKPIPKKGTVEGFEPADNKC LLRATDGGKKISTVSSKEVN* VFRWLISNPLGANMDGLKKR DKKNKTKKTKAAAAAAGP AAAAATAATTAATAAAQ
27150	57518	A	27313	1	1242	
27151	57519	A	27314	147	965	DPPSPVPAPPSPRDGHFLVPDA TMAEEQPQVELFVKAGSDGAK IGNCPFSQRLFMVLWLKGVTFN VTTVDTKRRTETVQKLCPPGEL PFLLYGTEVHTDTNKIEEFLEA VLCPPRYPKLAALNPESNTAGL DIFAKFSA YIKNSNPALNDNLE EGTPGKP*RFLDNYLTSPLPEEV DETSAEDERCLSDGTFLDGNEL TLADCNLLPKLHVQVVCCKY RGFHHPPRPFGRVAFGYLSNA\ YARENFRFPVPDDEEIELAYE QVAKALK
27152	57520	A	27315	1	933	

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27153	57521	A	27316	63	641	FAKMTDHHKGERGEATRYMFSR PFKKTMGVVPVCGHNN*RFYK/K GDIVD\IKMGYCVQNGMPHK CYHGK/GRSLTIVTPACLLPLL *TNQF*GKVF/SKRINVRIEHIKH ISKSRDSFLKRVKENDQKKKEA QEEGT\WVQLKRQAPPREAHF VRTNGKEPELLEPIPYEFHGIN RCPKKKIKDLWATKKKKK
27154	57522	A	27317	1	390	
27155	57523	A	27318	75	394	IWGDVEKGKK\IFIMECSQCHT VEKGGKHKTPNLHGLFRKTI GQAPWDPYTAANKNGIHWG EDTLMEYLENPKK\YIPGTKMI FAGIKKKEERADLIAYLKSSY
27156	57524	A	27319	2	529	FRQTRHAGGVRRGPRPKLQRD KAAAAAVLGAVRRKPSVVP AGQDPALSTSHPFYDVARHGIL QVAGDDRFGRRVVTFSRCRMP PSHLDHQRLLEYLKYTLQDY VENDYTIVYFHYGLNSRNKPS LGWLQSAYPEFDRKYKKNLKA LYVVHPTSFIKVLWNILKPLISH KFGKK
27157	57525	A	27320	287	445	
27158	57526	A	27321	2	362	
27159	57527	A	27322	30	365	EEAETVLVGQLKQLSSCLA/VH KYRPETKQEKQRLRLARAEEK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLVCRKMGVP YCIKGGKARLGRLVHRKTCTTV AFTQVN
27160	57528	A	27323	3	432	NSRVDDFVAQAQDAKGGKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ/RLRLARAEEKAAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVIAHDVDPIELV VFLPALCRKMGVPYCIKGGKAR LGRLVHRKTCTTVAF
27161	57529	C	27324	62	217	
27162	57530	A	27325	1	1545	

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27163	57531	A	27326	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRILYKRLKVPAINQFTQAL DRQTATQLLKLAKHYRPTKQ EKKQRLLAAREKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIADVDPIELVVFLPA LICKRMGVPCIIKGAARLGR VHRKCTCTVFTQVNSDKGA LAKLVEAIRTNYNDRYDEIRRH WGGNVLPKSPVARIAKLEKAK AKELATKLG
27164	57532	A	27327	550	827	DVSWAGRSEDHWRIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLQL PQEHTRKTLPLQQTSAWTYRLF HTSCEI
27165	57533	A	27328	908	1331	GDMRGREGGFGLRRTAMRC GCSPGVIREADNLVKLSPSTV RVTRSSASVMVLTMLAPATFL RVNCWAG/RGR/*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPKRDPL RVKDQGRHPCVV
27166	57534	A	27329	1	1134	
27167	57535	A	27330	62	310	
27168	57536	A	27331	243	578	
27169	57537	A	27332	324	995	NLVPRPGTWIRGLPLGDHSPVL LLFAP*ERSTYDLRSSDRPAQET SHQFQIRERQRRHVLSVDPKLR RRSRTGKAAFPWCLIIAGTPL*L YTHVSRVSDHAGMPALVLHP* R/LSPTFLGKGQHALKGLKPVIT RLQLHGLLKPINSPFPSPILPVLK PDKAYKLVQNLRLINQIVLPIHP VVPNPYTLSSIPPSTTHYSVLD LKHAFITPLHPSSQPLFAFT
27170	57538	A	27333	1	1860	
27171	57539	A	27334	1	957	
27172	57540	A	27335	97	826	
27173	57541	A	27336	245	392	
27174	57542	A	27337	736	1300	
27175	57543	A	27338	590	891	
27176	57544	A	27339	1256	1654	VQPVRLVSGMQHPGSGWRRLL WQGHSTSLTSKEHLHISKRGNI DNLVQRNMPASNEKPKCPFLPP FPSCLSTVHFIIIVVVQTVLFIGY IMYRSQQEAAAKKILLTIFLCT SSICVQNDVVLRFEKYLNCFIV
27177	57545	A	27340	295	852	

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27178	57546	A	27341	3	446	ILAWFGSIAEAPSAAWLCGSSQ GRYCSSFNVRVVRQNSSDAKV NVPKTRITFCCKVCGKHQPHKV TQYKGGKDSLYAQGRRRYDRK QSGYGGQTKPIFRKKAATTKKI VLRLCEVEPNCRSKRMLAIKRC KHFELEGDDKKRKGQVIQF
27179	57547	A	27342	1	565	
27180	57548	A	27343	1	1050	
27181	57549	B	27344	1	2109	
27182	57550	A	27345	2916	3229	
27183	57551	A	27346	3	671	AGILAAIREANMGAYKYIQEL W/RKKPSDVHAFLLRVRCGQT RSFFVFTGVPRPTRDPKARRLG YKAKQGYVYIRVRRGGRKRP VPKGATYGKPVHHGV\NPA*KF ASKALQVPLPEGTAGRHCGG S*ESLSYVWGDS\TYKFFEVI LIDP/YSHKAIRNPDTQ\WITK PVHKKHREMRGLTSAGRSRGL GKGHKFHHTIGGSRRAA WRRR NTLQLHRYR
27184	57552	A	27347	1	1646	
27185	57553	A	27348	2	2600	
27186	57554	A	27349	1	2403	
27187	57555	A	27350	100	520	
27188	57556	A	27351	1	570	
27189	57557	B	27352	1	837	
27190	57558	B	27353	1	1434	
27191	57559	A	27354	1	2379	
27192	57560	A	27355	3	952	IDWAPKSDRIVTCGADRNAYV WSQKDGVMKPTLVILRINRAA TFVKWSPLENKFVVGSGARLIS VCYFESENDWWVSKHIKPIRS TVLSLDWHFPNNVLLAAGSCDF KCRVFSAYIKEVDEKPASTPWG SKMPFGQLMSEFGSGTGGWV HGVFSASGSRLLAVVSHDSTVS VA\DAKSVQVSTLTKTEFLPLL SVSFVSENSVVAAGHDCCPMLF NYDDRGCLTFVSKLDIPKQSIQ RNMSA/LWERFR\NMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRFCTTGIDGAMTIW DFKTF\ESSIQGLRIM
27193	57561	A	27356	3	134	
27194	57562	A	27357	1	478	
27195	57563	A	27358	1	623	
27196	57564	A	27359	425	667	
27197	57565	A	27360	121	401	
27198	57566	A	27361	1	1818	

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27199	57567	A	27362	552	2325	
27200	57568	A	27363	693	1270	
27201	57569	A	27364	18	146	
27202	57570	A	27365	270	683	
27203	57571	A	27366	1	1398	
27204	57572	B	27367	1	1152	
27205	57573	A	27368	40	538	SPSPKDSPGVRVIGISCYIGGPCQ QRLLSPVVRASKMTKKRRNNGR A\KKGPRHVRGSPSLKFLPPSSC HLTVPRCRAQGTTRPIKKFVISK P*VEAAAVVRDISEASVFDAYL\ LPKLYVKLHYCVSCAIHKQK*S GNRS\RE\ARKTRTPPPRFR\PGG *LPHGPPTKSP
27206	57574	A	27369	204	401	
27207	57575	A	27370	3	980	
27208	57576	A	27371	2124	2836	
27209	57577	A	27372	139	8892	
27210	57578	A	27373	1	2592	MAGLGASLHVWGWMLGSL LAKAQVRASAPRHLFSRLRRG LSFSDTEARCARELIHVHTSTN APARTEAYPAGSAEPPRRRPRAG REHSFFSQRYVPLPPLGGALGS GPAKLPPPRAPCPVRFCADLET LCGALDCYKVRGGAAPARPAP RPAGGIQVSSLSGFGTESLPQGN PPPHRDHRESGTMDSPLTVAT PLSLTPPIPRELACGDWRRVGG GAGGGGLRRRLGGLGDKAGKR KSSDLP CGPGFLQSL LQKRRHW ESGLGLPGCGCELSVSGCGAP TLRQHIIIPAEGRNGVKEKSADL GCGGSQGLRAKKGTNPGIENG KRKGKEGMLDAWICRRSAFGP GREKLGGEVGCNDKGKIRFIE VKMSKKISGGSV VEMQGDEMT RIIWELIKEKLIFPYVELDLHSY DLGIENRD/ATNDQVTKDAAEA DKKHNVGVKCATITPDEKRV EFKLKQM WKS PNGTIRNLLGGT VFREAIJCKNIPRLVSGWVKPIII GRHAYGDQDQFGSNMQNAIMK KLKWLHLARVKGFS DANAKFY CRLYYAGEFHKMREVI L D S S E E DFIRSLSHSSPWQARGGKSGAA FYATEDDRFILKQMPRLEVQSF LDFAPHYFNITNAVQKRP LAKILGVYRIGYKNSQNNTTEKK LDLLVMENLFYGRKMAQVFDL KGLSRNRNVKDTGKESCDVV
27211	57579	A	27374	2	2138	

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27212	57580	A	27375	1	2355	
27213	57581	A	27376	249	1544	EIYSLSRFIEVKMSKKISGGSVV EMQGDEMTRIHWELIKEKLIFFY VELDLHSYDLGIENRDATNDQ VTKDAAEAIAKKHNHVGKCATI TPDEKRVEEFKLKQMWKSPNG TIRNILGGTVFREAIICKNIPRLV SGWVKPIIIGRAHYGDQYRATD FVVPGPVKVEITYTPSDGTQKV TYLVHNFEEGGVAMGMYNQ DKSIEDFAHSSQMAKSGWPL YLSTKNITLKKYDGRFKDIFQE MYDKQYKSQFEAQKIWEYHR LNDMDMVAQAMKSEGGFIWAC KNYDGDVQSDSVAGGYGSLG MMTSVLVCPDGKTVEAEAAH GTVTRHYRMYQKGQGDVHIP LASIFAWGPEGLVAHRAKLDNN KELAFFANALEESFYETHEVAGF MTKDLAACIKGLPNVQRSDYL NTEFEMDKLGENLKIKLAQAK
27214	57582	A	27377	1	692	
27215	57583	A	27378	251	2150	
27216	57584	C	27379	93	293	
27217	57585	A	27380	308	534	
27218	57586	A	27381	2	856	
27219	57587	A	27382	3	327	AQELHIFTEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCQGEALTTLEVAGRM LGGIAKQEKKKKKTGRAKRRM QYNRRFVNVPFTGKKKGPNA
27220	57588	A	27383	150	456	
27221	57589	A	27384	651	835	
27222	57590	B	27385	1	2193	
27223	57591	B	27386	109	714	
27224	57592	A	27387	150	458	
27225	57593	A	27388	1	2055	
27226	57594	A	27389	1	804	
27227	57595	A	27390	645	1828	
27228	57596	A	27391	899	1216	
27229	57597	A	27392	79	156	
27230	57598	A	27393	1796	2215	
27231	57599	A	27394	107	724	
27232	57600	A	27395	854	926	PLEIPHEPPPRG*HAPQLPRGQ
27233	57601	A	27396	2	413	
27234	57602	A	27397	54	442	FAKMTNTNLNRRGTRYMFSSRP FRKHGVVPLATYMRIVYKGGDI VHIKMGTVQKGMPHKCYHG KTRGVYVNTQHAVGIVVKNQKQ KGGILAKRINVRIEHITHSKSRH SFLKRAKENDPEYEALENGT

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27243	57611	A	27406	142	1285	SRMSKAFGLLRQICQSILAESSQ SPADLEEKKEEDSNMKREQPR ERPRAWDYPHGLVGLHNIWT DLACLNSLIQVFMNVDFTRIL KRITVPRGADEQRRSVPFQML LLEKMQDSRQKAVRPLELAY CLQKCNVPLFVQHDAALQYLK LWNLIKDQITDVHLVERLQALY TIRVKDSLICVDCAMESSRNSS MLTLPLSLFDVDSKPLKTLAEDG LHCFQPRELSSKSKFCFCENG KKTRGQKVLKLTHTLPTLTIHL MRFSIRNSQTEKDLATPLYFPQS LDFKPRSFQKRESCDAEEQS GGQYELFAVIAHVGMADESGHY ICVYIRNAVVGKWFVCFNDSNIC LVSWEIQCTYGNPNYHWQET AYLLVYMKMEC
27244	57612	A	27407	1	1077	
27245	57613	A	27408	3	242	
27246	57614	A	27409	213	928	EGPARQLLSPVRASKMTKKR RNNGRAQKRAAAHVGRGPSPLK/ CFPSGPLPPNCAR/CVPGQTRPI KKFVIRINIVGGRSRQGHISEAS RLRMPISLPLKLYVKLHYCVSC AIHKQK*FR/NRS/RESPAKTRTP PPRF*DLAGGCPTVPPKAHDL GPEYCRHQTCVNVWCCRQATI LGKELCGQIRKLPSQQMSPGWL PSGYSCWLKYKTEATTALQS RGEVYHPLQALWSRPPGRDPL
27247	57615	A	27410	1	267	
27248	57616	A	27411	257	322	
27249	57617	A	27412	2	176	
27250	57618	A	27413	218	923	
27251	57619	A	27414	2	429	TKFAARRPALAACAAISKIKAR DLRGKKKEELLKQLDDLKIVE LSQLRVA*VTGGAASKLSKIRV VRKSIARVLTIDNTSGKKTFR EILTRGKKYKPLGPCGP*GRTR AMRRRLNKHEENLKTKKQQRK ERLYPLRKYAVKA
27252	57620	A	27415	1	1146	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
27253	57621	A	27416	2	670	IAGEITRRGSRARPRPGPQCPPG PPGTAMIKAILIFNNHKGPRLSK FYQPYSED TQQIIRETFHLVSK RDENVNCFLEGGLIGSDNK/ LIYRHYATLYFVFCVDSSESEL GILDLIQVFVETLDKCFENVCEL DLIFHVDKVNILAEVMVMGGM VLETNMNEIVTQIDAQNKLEKS EAGLAGAPA/RAVSAVKNMNL PEIPRNINIGDISIKVPLNPSFK
27254	57622	A	27417	5	379	
27255	57623	A	27418	536	675	LEWSSAKFPTAVGVSLLSVVC RSQ*FLMDAMSMDLVRYTSA RVS
27256	57624	A	27419	2	1220	
27257	57625	A	27420	435	552	
27258	57626	A	27421	5	379	
27259	57627	A	27422	1	1062	
27260	57628	A	27423	17	467	
27261	57629	A	27424	105	355	
27262	57630	A	27425	283	466	APRSARPIVHG VKATRPKPRNL LDKDMFSKSDPLCMYTOGME NKQWR/EFGRTVIDNTLN
27263	57631	C	27426	167	379	
27264	57632	A	27427	164	1185	
27265	57633	A	27428	1	873	
27266	57634	B	27429	20	523	
27267	57635	A	27430	3	1225	
27268	57636	A	27431	1	884	GTRDATAEENRVLLAMVNPTV FFDIADVGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGSSIFITS D*KNSCLPLIVQQCLFLRLPL FADKVPKTAENFRALSTGEKGF GL*GVPCFHRHIFGM/CQG/GDF TRHNGTGGKSIYGEK/FEDENF ILKHTGPGILS/MANAGPNTNG SQFFICTAKTEWLDGKP/VVFG KVKE/GMNIVEAMERF/GS/RNG KTSKKITADCGQLRIKFDLVF YSLTTKIIPSGSPRESTPPTLLA SILESLCSRLQFPFGFHVFLVPS
27269	57637	A	27432	27	410	LQDEATGCKLIEVDDERKLRT FYEKRMATEVAADALGEEWK GYVVRISGNDKQGFPMKQGV LTHGRVRLLSKGHSCYRPRRT GERKRKSVRGCIVDANL/SVLN LVIVKKGKEDIPGLTDTTVPR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27270	57638	A	27433	93	866	TVSFPATGCGQLIEVDDEKRL RTFYEKRMATEVAADALGEE WKGYYVVRISGGNDKQGFPMK QGVLTGHRVRLLLSKGHSCY RPRRTIGERKVRKSSSVGCIIVDS KSWSVLQLGLLLKKKKK*RRIF PGLTDTTVPRLGPOK/RASRIR KLFNL SKIEDDVQYVVRKPLN KEGKKPRTKAPKIQRLVTPRVL QHKRRRIALKKQRTKKNKEEA AEYAKLLAKRMKEAKEKRQE QIAKRRRLSSLRASTSKSESSQ
27271	57639	A	27434	2	401	
27272	57640	A	27435	1373	1838	
27273	57641	A	27436	1	257	MNRQLSDSYTEDTKEPSDVTT ETRSPPGSAKTTMIDTLKKLQ DVQKLRTPKIPQSQQICWNN MSRLRDQS*RSSKKRQLWK
27274	57642	A	27437	247	831	
27275	57643	A	27438	1	993	
27276	57644	A	27439	267	281	CNCPNIFEARWVNLKSLSKIHE* RPFQP
27277	57645	A	27440	274	482	
27278	57646	A	27441	1	219	
27279	57647	A	27442	1	681	
27280	57648	A	27443	11	1094	
27281	57649	A	27444	51	65	NNTFLKYC*IDFND*DCGGEDIS PN*LGLPIPLSMVLCEIHF
27282	57650	A	27445	1	1563	
27283	57651	A	27446	3	318	
27284	57652	A	27447	1	294	
27285	57653	A	27448	7	259	
27286	57654	A	27449	29	191	
27287	57655	A	27450	2	519	KSQDYKSLNATCAGTGSFGC ARRLLSTCSSGWRSGGLSLRG GKMELEA/MSRYTQPSEPQLSS PHLTVVLLAIGMFFTAWFFVY EVTSTKYTRDIYKEAPHPP*VA LTPSMGGVLFALLWVGYYRV SHPRVTTQNGFHWKPAFCKINF FFYLF AWEVFPPAAHNKVQML
27288	57656	A	27451	144	386	VCECKMPKVQPNFTHWSRS*N DDLNRSSLWQA*PQAASVEIHL RS
27289	57657	A	27452	462	672	
27290	57658	A	27453	1	475	
27291	57659	A	27454	1	741	
27292	57660	A	27455	62	390	
27293	57661	A	27456	549	641	
27294	57662	A	27457	456	774	
27295	57663	A	27458	2852	2935	

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27296	57664	A	27459	699	761	
27297	57665	A	27460	399	434	
27298	57666	A	27461	683	1661	
27299	57667	A	27462	1	95	
27300	57668	A	27463	3	517	
27301	57669	A	27464	6	401	RGLTEVPETSGGRVSVGAMAK HHPDFLCRKQAGVAIGRLCEK CEGKCVICDSYERPTLVRICDE RNYGSYQGRVCVCGPGVSDA YYCKEVHHPGERTRDGCSKIV NLGSSKTDLFL* TAKNTGFQER
27302	57670	A	27465	1	321	
27303	57671	A	27466	67	348	
27304	57672	A	27467	1	642	
27305	57673	B	27468	193	445	
27306	57674	A	27469	32	216	AGPSQPTNQTTGKSPQLQQDYF PRRSYRCSHRLIICLVNIGDAV* STVQLKALMLRGRNYK
27307	57675	A	27470	214	440	QDRWGLAPHPPAPGLPLPGPTN QTTGKSPQLQQDYFPRRSYRCS HRLIICLVNIGAL*STVQLKAL MLRGRNYK
27308	57676	A	27471	35	3801	
27309	57677	A	27472	1	2901	
27310	57678	A	27473	1	1317	
27311	57679	A	27474	1698	3255	RVACPCVVWLCWAHWELWRT EEVEGGIAGTDVAR/EASDFILT DAIFSSIVKAVMASLQRRGSRE L*LPAAGVWKLQTD* AQS/ AE EGIECKSIKPVLA KYLVWTRLF VGLLAELRDESAPETTPAGRRR QPQVWSGARQTCGQRTERLAG GLGEMQACSGNLGAEKEKQSK KLAGGWPMSPSTLHALGPKLV PAKSQRRHRAEHMSTWQVGVVS SSYFTGNLVGTLTGYVVIKRGF NRSYYLASFIFAAGCAGGLMI GFWSWLA WRFVAGVGCAMIW VVVESALMCSGTSRNRGRLLA AYMMVYYYVGTFLGQLLVSKVS TELMSVLPWVTGLTAGILPLL FTRVLNQAEHNDSTSTSMKL LRQARLGVNGCIISGIVLGSLYG LMPPLYLNYKGGKSSPTAVRPA RHNSLPGPEAKKYRPGFIGLTS CIAFSVQAANVDEYITQLPAGA NLALMVQKV GASAPAYDHSQ QMALPASTQKVITALAALQLG PDFRFTTTLETGKNVENGVLKG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in U.S.S.N. 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27312	57680	A	27475	152	468	GLGIQ*LLCCSSFCQLLPEKKE GRLAGDAGAARPAKSGRFLGL TSGLPSEWSARTGPEPPKSLSG GGELNGSSLGFGTQDGRGTRE GRDRGLHPARPPQYQHSP
27313	57681	A	27476	541	4172	
27314	57682	A	27477	3	1110	
27315	57683	A	27478	340	1032	
27316	57684	A	27479	2	779	
27317	57685	A	27480	3	281	
27318	57686	A	27481	519	737	VPDLLQLPNAGLCGHFCDPGD SLQCCLCHQGPFGQAQNWAAV WADTKPAAGAEAREPGDLA*L VPPTWSPTR
27319	57687	B	27482	1	915	
27320	57688	A	27483	68	145	
27321	57689	A	27484	1281	1433	
27322	57690	A	27485	171	708	
27323	57691	A	27486	1	270	
27324	57692	A	27487	278	588	VYIKRMPKKKV/SEGTIKEPKR RLAQLSAKPAPAKVEAKLKKK AAKDKSSGKNVQTKGKRRK GKQAKVANQETKEDLPAENGE MKTEESPASDEAGEKETKSD
27325	57693	A	27488	304	513	PVRHGAFFQDKSSDKKVVQTKG KRGAKGKQAEVANQETKEDL PVDISGETKTNEESPSSLIEAGEK EAKS
27326	57694	A	27489	1	435	
27327	57695	A	27490	3	273	
27328	57696	A	27491	9	293	
27329	57697	A	27492	1	504	
27330	57698	A	27493	1	529	IPPPRLFLPVATEVARVRLPPPP PPQNAARDALTSPSYLAWASPR KQTPSPPAAKDIKILEQRGYP KADDDR/LNKVISEAEWKYTL KDVIAPGVLASLPSVPAAGGAV AVSACPQALAAPCCLGSAPA/A AEGEEKMKKKEEVLKES/DDD/ MGFGPFELKSLPPLQIKGLFYTS R
27331	57699	A	27494	1	396	
27332	57700	A	27495	2	398	
27333	57701	A	27496	1	702	
27334	57702	A	27497	1060	1446	
27335	57703	A	27498	46	216	HPLQLSVIPFLPVK*HVDQMFG AD/CVLSN*VNCLASRLFAVSV ALRSSRFITMVP
27336	57704	A	27499	1	1152	
27337	57705	A	27500	126	184	
27338	57706	A	27501	238	498	

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27339	57707	A	27502	1	852	
27340	57708	A	27503	3	171	
27341	57709	A	27504	1064	1302	
27342	57710	A	27505	449	668	SPGDYFISLMAAMGRPQVGWY APELLQKMMRKRMR/VKKLI QNYKQLK/CSLT.LNNHVKLVRT NLRFHLAGLLG
27343	57711	A	27506	1	2454	
27344	57712	A	27507	2	408	
27345	57713	A	27508	205	715	
27346	57714	A	27509	1	813	
27347	57715	A	27510	1	864	
27348	57716	A	27511	17	396	
27349	57717	A	27512	3	428	LTNYAAAYCTGLLLARRLLNR LGMDKIYEGQVEVPNGEYNVE SIDGQPGAFCTCYLVADLARTTT GNKVFGAPEGAVDGGLSNPHS SKRFLGLSIPHSK*ILGYDSEN KEFNAEVRKRHIMGQKFADDL HCLIEEDENASKK
27350	57718	A	27513	164	431	EFFFTSNIGVYLQIIHVGKPI*H /YLV*ILSY*HLAARTISSKIKSN SLVPCASNRGDVGSTRPRVTR RSVRYSAAPLRSPFLAR
27351	57719	A	27514	1307	1947	TNEGSGNSAPLFSGARNQTRMI VRGTNR/DIICQIAYARTEGDMI VCTAYVHELPHYGVKVDLTNY AAAYCTGLLLDRLLNRDFMD KIYEGQVEATGDDYNVVSIDG QPEVHRKHIMGHNVADYMCY LMEEDEDGYKKQFSQYMKNSV TPDMMEEMCKKAHAAIRESV CEKKPKKEVKKKWNRPKMS LAQKDWVAQKKASFLRAQE RAAES
27352	57720	A	27515	1	987	
27353	57721	A	27516	1521	1641	
27354	57722	A	27517	2	614	ILSRVVEFPLTAEVPPPELLAAAG FFHTGHQDKVRCFFCYGGLQS WKRGGDDPWTEHAKWFPSCQFL LRSKGRDFVHSVQETHSOLLGS WDPWEEPEDEPLWPPPSLPLG TLSCPHGERSSLKVPFSQEGSV QPRPRGRGGFLSPQ/DARDVEA QLRRLQEERTCKVCLDRAVSIV FVPCGHLVCAEACPLQLCPI WQKPPSRSR
27355	57723	A	27518	3	89	

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27356	57724	A	27519	1	1618	ASSHVETRAHAERLLKKLFSG YNKWSRPVANISDVVLVRFGLS IAQLIDVDEKNQMMTTNVVVK QEWHDYKLRWDPADYENVTSI RIPSELIWRPDI VLYNNADGDFA VTHLTKAHLFHDGRVQWTPPA IYKSSCSIDVTFFPFDQONCTMK FGSWTYDKAKIDLVMHRSVD QLDFWESGEWVIVDAVGTYNT RKYECCAIEIPDITYAFVIRRLP LFYTINLIIPCLISCLTVLVFYLP SECGEKITLCISVLLSLTVFLLLI TEIIPSTSLVIPLIGEYLLFTMIFV TLSIVITVFVLNVHHSRPTHMT PTWVRRVFLDIVPRLLLMKRPS VVKDNCRRLLIESMHKMASAPR FWPEPEGEPPATSGTQSLHPPSP SFCVPLDVPAEPGPSCKSPSDQL PPQQPLEAEKASPHSPGPCRPP HGTQAPGLAKARSLSVQHMS PGEAVEGGVRCRSRSIQYCVPR DDAAPEQMARLPAPWPLATPT RLSSHPQTSPLRANAHARRSPL RCPRVPRSRPAAPKHRPRTCCP
27357	57725	A	27520	1	3158	
27358	57726	A	27521	2	237	
27359	57727	A	27522	76	254	PLHITFFSRACFPSLHNCCHEY*Q PGF*TSKTPQLWCQLRQYSFK HSFLVVP TPCVPLLG
27360	57728	A	27523	86	376	SLEGRLSDYTPTFQGCQTQGR LPWSFTLSGKSRFSGEGARACY KCQKSDHQARNACSPGFLLSRI PSVRDPTGNRTVQLTWQPLPEP LELWPKAL
27361	57729	A	27524	1	167	MPEPQRPGVPEPPPPGACYAC RKSGHWAARNARSPGFLLSRVP SPPGPSRTPSFG
27362	57730	C	27525	1	381	
27363	57731	A	27526	243	437	VTSTVRQTPATSPAHNKFMPE PQRPGVTPEPSPGACYKCQKS DYQARNACSPGFLLSRVPVS
27364	57732	B	27527	88	1485	
27365	57733	A	27528	1	3759	
27366	57734	A	27529	36	438	RNDRVRPHRDVYSLQGRLSDH SPTTFQGCQTQGRLPWSFTLSG KFRFSGEGATTSPAHNKFTPE PQWPGIPPEPPPTGACYTCRKSG HWAARNARRPGFLLSRIPSVWD PTENRTVQLTWQPLPELELWPKAL

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27367	57735	A	27530	314	691	SLQGHLSDYTLTFQGCQTQGH LPWSFTLSGKSRFSEEGTKGDV SGSQDNCGERVSRQTRQRLSH HRQGACYTCRKSGHWAIRNAR CPGFLLSVCPSVWDPTENRTVR LTWQPLPEPLELWPKAL
27368	57736	A	27531	383	2907	RSPTSKTKDICHRSWRRGL/WV NKASEGDELDLRDVSVASNIEP WTGWCRAPLQADLGNSSSA SAPPPYNPFITSPPHWGLQFR SVTSPPPAQQFTLKKVAGAKG IVKHALKRLKPVITRLLQHGLL KPINSYPNSPLPVLKPDKPYKL VQDLRLINQIVLPIHPVLGIIGLT SSVRRDAGQDLKRDRAEFLIG DEVHHPHRRRIAEARRLLLGQH FDPLHRLIGQVLEGEARYAPP VEQHRLAPARRTGQRLHPL QFQAGRAQRNRNLGIEHRDR LDRPDDGAGNALAGDGFRRG CLFAGIGIRPRYCRYRQSQDDR RPSHAAPRPRALPIHPATPIA DVMVMFSAVMSQLRLVLRHI DGISRWPPAVVFITDVKIWL VY PSDDCRIRSNDRDDMQGEAPA MSMNAAARVGDPIGHSFSQGL FGEALDGLFFARRSEVDMRAG NLGRILARGLSGGRWTPADGQ LTLGSRDVFINGPPATMTIRSTG QCRQHSGLRTVTRTETDSIGPIE VPADAYWGAQTERSENFPFG AREQMPIGIVHALAIVKKAAR INRGHGLAGEKADAIESAAHDV IEGRHDDQFPLVIWQTGSGTQS NMNANESSNDTFPTALHYAAA LAVTKQLFSALDRHLAALDAK AKEWDSIVKIGRTHLQDATPLT LGQEFSGYVQQLANARDRIEGL
27369	57737	A	27532	929	1227	PENGTTFESILQVLDNSCHKMG KWS/RGA*RPGILLHIGPSLVSA PNVTHPKSFFFLSFLFRSPQV PSPLNPSFLWTHLTSPL.LPRL.LL ARLSQVPILT
27370	57738	A	27533	98	412	LGSGLPWEINPLSSCSLLCEKH PPITSGPQTDQPKKHLTNFKSG ACYMCRKSGHWA/RANARSPG FLLSRIPSVWDPT*KFGLVQLTL GKPLPEPLELRPLRLSD
27371	57739	A	27534	14	249	
27372	57740	A	27535	49	341	
27373	57741	A	27536	392	371	

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27374	57742	A	27537	1	1590	MPNGTNEISHRYNASERSQTKQ DEQTKGTVGPPEWTPLVRRNG GDSGLDFHFFAEKLIKIIIVDSAG RAGTGHRMPAPVHFGHRGQA MITLSPLRAKQKAVLQKPPPLT STYSLMLPLFLPDKRPPTTEWF LPVMEADAHELTLAWLMLALYR KPNASVQGSQAETLCVFRVKE PLEWQALFADVHSGVNDKGP INCSLYEHKINVSEIVLNLAQTQ KNPAHSDPSSTPAGCMVGTTA GGSVMSACCPSPAAPGPLPGP ATGSC/SPSAAPRPDPPPP GIMAIRAAPSCLGACITLQDEET CEQTHTHSRIMYILFARCLLH AIARGRSRKCAASAGGTCPIHVR VPGGGSYFRVSLQGGQTHWMR PENGFTCVRTKSRRCPIIREQH PTKIPKALTANANQAFFLLVNG HSMVASPHQSQRADLGGFWR DASSLLANSQVQVCGSLRKR HGWWVPFSLRCAVPLTADDSR LRTASLEMSTPPMIHVQDDWQL RRGLPAGTAVTVSELIYLNAN GRLQVEKFLF
27375	57743	A	27538	279	759	
27376	57744	A	27539	443	696	
27377	57745	A	27540	1	179	
27378	57746	A	27541	3	1237	
27379	57747	A	27542	4	152	
27380	57748	A	27543	760	908	
27381	57749	A	27544	203	570	
27382	57750	A	27545	312	500	
27383	57751	A	27546	1	441	
27384	57752	A	27547	1	630	
27385	57753	A	27548	1	1254	
27386	57754	C	27549	236	408	
27387	57755	C	27550	220	398	
27388	57756	C	27551	254	445	
27389	57757	A	27552	1	2742	
27390	57758	A	27553	1	744	
27391	57759	A	27554	1135	1751	RPGSTLQVRQNYHQGLRRPPIN RQINLELYASIVVYLSMSYVF DRDIDVALKNFAKYFLHQSHE EREHAET**KLQNRRLAEF FLQDYQRNQD/CDDWGRAGLN VAMECALAFWKKNVESHYV NLHKLAT/DKN*PPIWCDFHV RHIYLE*AG*KAIRIWGDHVN QTFA/RKMGSAPNLGFGLEYLF* QSTPWGSDNESSPWG

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27392	57760	A	27555	224	547	
27393	57761	B	27556	22	130	
27394	57762	A	27557	1	408	
27395	57763	A	27558	1	1011	
27396	57764	A	27559	56	822	
27397	57765	A	27560	146	411	
27398	57766	A	27561	1	885	
27399	57767	A	27562	115	1200	
27400	57768	A	27563	791	1114	
27401	57769	A	27564	67	401	RLGSSGREVIHPGERGLENNVC/ H*SSGNQENELEMNKTANGDC RRDPRESRSPIERAVAPMTSLH GSHLYTSLPSLGLLEQPLATKN SLDASRPAGLSPTLATPGERQQN
27402	57770	A	27565	109	345	HPLFIFFDPLPPTFFHPLIGPRMC FSPGLALCPHPNLILNCSSHNSY VLWEGPGGK*FESWGRFPDHT VLVIVNKSHKI
27403	57771	C	27566	63	167	
27404	57772	A	27567	231	314	
27405	57773	C	27568	99	323	
27406	57774	A	27569	1	1347	
27407	57775	A	27570	192	269	WFYKGEFLCTHS/HCLLPKRTC LLPAAM*YCDQFSMAGETSQS WQKAKEEQRHILHGGQRKARL TWQQAGECVHRNSPL
27408	57776	A	27571	107	797	AQWRRAAPPAAGVTCFRLQP GMETPLDVLRAASLVHADDE KREAAALRGEPRMQTLPVASAL SSHRTGPPPIPSKRKF*SMEP*G DEDLDCDNDHVSCKMS*RIQPPI LNKTANGLRLARRDPRESRSP ERAVAPMTSLHGSHLYTSLPSL GLLEQPLATKNLSDASRPAGLS PILTPGERQQNRPSVITCASAG ARNCNLSHCPIAHSGCAAPGPA SYRRPPSATCV
27409	57777	A	27572	1	1686	
27410	57778	A	27573	1	1614	
27411	57779	B	27574	208	366	
27412	57780	A	27575	15	1729	
27413	57781	A	27578	1	1614	
27414	57782	A	27579	308	464	KAHHHWLEKCKSEPQ*DTISW TWMKLETHILSKLPQEQKTRNC MFSLISGS
27415	57783	A	27580	291	378	
27416	57784	A	27581	2	91	
27417	57785	A	27582	439	519	
27418	57786	A	27583	2	91	
27419	57787	A	27584	2	91	
27420	57788	A	27585	2	91	

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27421	57789	A	27586	50	394	
27422	57790	A	27587	1	666	
27423	57791	A	27588	2	91	
27424	57792	A	27589	5	91	
27425	57793	A	27590	884	991	
27426	57794	A	27591	290	460	
27427	57795	A	27592	86	349	
27428	57796	A	27593	2	89	
27429	57797	A	27594	723	882	
27430	57798	A	27595	255	352	TGTWMKLETIILSKLTQE/QKTK HCMFSLISGS
27431	57799	A	27596	1	1685	
27432	57800	B	27597	82	263	
27433	57801	A	27598	491	816	RHRGAQRKAFLQRVNCGLCCT WNLCPOKLRGRK WPVQVSPA AGRDPGGPLL*PEGTLWGAPFC LGAPPPLLTAAAPAGRAGGT RGAAPACPEDRTNAHSQHHP HV
27434	57802	A	27599	645	1142	
27435	57803	A	27600	218	326	
27436	57804	A	27601	181	2316	
27437	57805	A	27602	2	238	
27438	57806	A	27603	709	1416	
27439	57807	A	27604	3	501	SSRALRLLGVVVRIRQAGTMA VTKELLQMDLYALLGIEEKA DKEVKKAYRQKALSCHPDKNP DNPRAELFHQLSQALEVLTDA AARAAYDKVRKAKKQAAERT QKLDEKRRKKVKLDLEARERQA QQQGE*GGRRESRSTRLEQEIE RLREKGSRLQEEQRLI
27440	57808	A	27605	1	963	
27441	57809	A	27606	135	384	
27442	57810	A	27607	349	679	SETYWFPPRESQHLDLDVWPPR SEHHSQSTGTHSGVSESLSPRYF QRCNAHSPSQGHIEEQYLAPWK HRLYQRMSDLPLNDR*FQYSK GHHRCSQNEAVQNPQQLQSL
27443	57811	A	27608	1590	2758	
27444	57812	A	27609	123	2312	
27445	57813	A	27610	1	1809	
27446	57814	C	27611	79	309	
27447	57815	C	27612	77	325	
27448	57816	A	27613	1	606	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, /=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
27449	57817	A	27614	2	686	SQCAELASAPLSPAPGLPRHSRL HALLGLAMPVDLSKWSGPLSL QEVDEQPQHPLHVTYAGAAVD ELGKVLTPQVKNRPTISWDG LDGKLYTLVLTDPDAPSRKDP KYREWHHFLVVMNMGNDISS GTVLSGIVGSGPKGTGLHRY VWLVEQGRPLKCDEPILASNA RSGDHRGKIQRWASLPVKKIYE APGPPVAGHRVTPSPKWDEPM CPQTVTKQLSWGK
27450	57818	A	27615	446	1300	
27451	57819	A	27616	2	346	
27452	57820	A	27617	1	305	MAISTGSSVPWPSPA/PSGPHGR GSPWGFCLATCWQSIGRGQGD PWSAGSGHPGTKGASAPGPGE GQSGGDSGSA/GR*GSHHLPGP ASFRAGSGQAWDGKKG
27453	57821	A	27618	287	475	
27454	57822	A	27619	37	314	
27455	57823	A	27620	1	367	
27456	57824	C	27621	360	610	
27457	57825	A	27622	604	980	
27458	57826	B	27623	8	442	
27459	57827	A	27624	1	2268	
27460	57828	A	27625	296	398	APPGPTLPWASTPSRGCT*APPG PTLPWASTPSRGCTSSWFMLPA MRRCGAPC
27461	57829	A	27626	1	3633	
27462	57830	A	27627	1853	3809	
27463	57831	A	27628	1	656	MTHNQEKNKSTNTEMTMMMK LADKDDKTAMINMLQVVKV EEAMSMRRNKDVKNHGRA RWVKPMIPALWEAKEVEGKYS AHNFWGSWKFSSSSSSSGPE SPARTHASFQPDGPTNKLGT KAFRVSPASSLLVDLNTQVEII NVRKATPTCSLELGRKRRDGA AERAALDVVVVIYQLAPAAAP NCLNPVTSRR/PPQTPAPEGQGR RQSFE
27464	57832	A	27629	127	273	
27465	57833	A	27630	3	405	AAFHARGHRAGLSASSCSWRC CPSSAPCAPYAAPAARMLQTC LKQSPAGMPPASPSPAASHWG STSFYSYSPRSTSTSCCPICSSW ESWPCPTPSSPL*NKFFPASFPN RQYQLLFTQSGSNGEKDHL
27466	57834	A	27631	689	987	
27467	57835	A	27632	228	527	

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27468	57836	A	27633	108	441	
27469	57837	C	27634	156	287	
27470	57838	A	27635	2	363	RFTKVEKMK/MLSAAREKGR VTHKGKPSLKAADLSAETQAR REWGPFINLKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKALNMERNNW YQPLQKHAKL
27471	57839	A	27636	2	367	
27472	57840	A	27637	1	936	
27473	57841	A	27638	1	865	
27474	57842	A	27639	1	1287	
27475	57843	A	27640	1	2565	MGPGARLAALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLRRYLRGEEARLRL TRCNDETITYLLDKRLTVLTA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLSRWAVGGATG SWVLSKGDRAASGERVVTGWA TLNVGRSFAYCLTTCVQPLDV GPRKEHAPRPPSLPTSTRQGRQ SERSQDANGRRKQKTKSEPERF EDAVLLAGFKVEEPPVQPRRK EWFQGPSPGHCCPAQPDASAPC ILATHAPARAQNA PGTA WAAA LEGTS TVSLDHFHVVG VVVVS GGEIILL SFRFYDKVLSLHEDS TTPVANPLLAFTLIKRLQSDWR NVVHSL EASENIRALKDGYEKV EQDLPAFEDLEGAARALMLRQ DVYMLNVKGLARGVFQRTGS AITDLYSPKRLFSLTGDDCFQV GKVAYDMGDYYHAIPWLEEA VSLFRGSYGEWKTEDEASLED ALDHLAFAFYREQSSPATEQS WMENDFDELREEGFRRSNYSE LQEEIRNTNGEVKSFEEKLDEW ITRITNAEKS LKDL MELKTKAR ELRDECRSLSSRCNQLEERSV MEDEMNETKRGKFKREKRIRK NEQSIQEIWDYVKRPNRLRIGV LESRENGTKLENTLQDIQENF
27476	57844	A	27641	219	451	APAAEGAGRIS/PCSRHSPAGLE/ WLCPLCALF*QCPP/PTCHQSA SPR/WP*G/RPAAGPHPPAATVA PKRKGKTKSSSTRE
27477	57845	A	27642	237	561	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
27478	57846	A	27643	3	461	TRTRRGSRTAEAR*CTPGWRPA GRRSALCSRGLGP*RPPTRS GAAPGPHSPCGRPDGPACSRLP PHRSRSPPHGSHVPAAGWLSAG PHQRWPAAGPGTDQCRVVG PERASPHIWKGSTVPFLPSWIFL RVLSVPGCSLPRCCWLGHQC
27479	57847	A	27644	2	159	
27480	57848	A	27645	1	243	
27481	57849	A	27646	219	462	
27482	57850	A	27647	256	427	
27483	57851	A	27648	1	954	
27484	57852	A	27649	2	4690	
27485	57853	A	27650	1	1275	
27486	57854	A	27651	1	867	
27487	57855	A	27652	1	472	
27488	57856	A	27653	2	1215	
27489	57857	A	27654	3	401	
27490	57858	A	27655	712	1245	
27491	57859	A	27656	2	1178	
27492	57860	A	27657	278	339	
27493	57861	A	27658	1	1407	
27494	57862	A	27659	1	687	
27495	57863	A	27660	484	776	
27496	57864	A	27661	299	1318	
27497	57865	A	27662	1	960	
27498	57866	A	27663	122	282	
27499	57867	A	27664	1	600	
27500	57868	B	27665	1	375	
27501	57869	A	27667	356	439	
27502	57870	A	27668	49	360	
27503	57871	A	27669	2	580	GRVCGGPWAARVGERIPNMA GRKLAS*KPTD*VAFARD/IIPQ NPKAPLPSFLKS/WNGDPSPSRL AALP*ESHPAIDWA*LPRPNVA QGLAWVDDFE/KKFNAERFPC PEDK/YTAQVDA/EEK/EDVKS C/AEWVLSKA/RIVEYEKEME KMKNLIPFDQMTIEDLNEAFP ETKLDKKKYPYWAHQPIENL
27504	57872	A	27670	1	675	
27505	57873	C	27671	137	1357	
27506	57874	A	27672	1	1032	

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27507	57875	A	27673	3	938	MANNPGANGQ\PGGPGGPGMG KPRCF/RGEVFGIVIRGRGSR/R GRGRGR\GRGARGSKGRG*RD WVPVHVQVGAALVKDH*RSKF PWKEIYLFSLPH/IKESIIDF\FL GGLLSKDEGFE*LCPVQEQ\TRA GPAATR\FKAFCCYPGTNGJIV GLGVKCSQE\VAHRPFRGAML AKLSIVPVVR\RGYWGNKIRKP\ HTVPICKVT\GRCGSVLVRLIP/S QPRGTGIVSAPVVPNKLLMMAG IDDCYTSARGICTATLG\NFAK ATVFD\AISKTYSYLTPDLWKET VFTKSPYQEFDTQLVKDHTRVS VQRTQAPAVATT
27508	57876	A	27674	1	864	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLLAMVNPMTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIGL\FADKVPKT AENFHALSTGEKFGFYKGSCFH RIIPFGMCQGGDCE/RHHNGTG GKSIYTEKFEDENFILKHTGPGI LSMANAGPNTNGSQFFICTAKT EWLDGKHVLF\GKVKEGTNIVE AMERFGSRNGKTSKKITIADCG QLLISLTCVLS
27509	57877	A	27675	2	752	
27510	57878	A	27676	3	327	AQELHTFEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCGVEALTTELEVAGRM LGGVAKQEKKKKKTGRAKRRM QYNRRFVNVPVTFGKKKGPN
27511	57879	A	27677	567	838	

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27512	57880	A	27678	3	1923	ATMAQGLEVALTDLQSSRNNV RHHTTEITVDHLLVRRGQAFNL TLYFRNRSFQPLDNIHFVETE DAVYLDSEPRQOEYVMNDYGF IYQGSKNWIRPCPWNYGQFED KIIDICLKLDDKSLHFQTDPATD CALRGSPVYVSRVVCAMINSN DDNGVLNGNWSENYTDGANP AEWTGSAVILKQWNATGCQPV RYGQCWVFAAVMCTVMRCLG IPTRVITNFDSGHDTDGNLIIDE YYDNTGRILGNKKKDTIWNFH VWNECW MARKDLPAYGGWQ VLDA TPQEMSNQVYCCGPASV RAIKEGEVDLNYDTPFFVSMVN ADCMSWLQGGKEQKLHQDT SSVGNFISTKSIQSDERDDITEN YKYEEGSLQERQVFLKALQKL KARSFHGSQGAELQPSRPTSL SQDSPRSLHTPSLRPSDVVQVSL KFKLLDPNMGQDICFVLLALN MSSQFKDLKVNLSAQSLLDHG SPLSPFWQDTAFITLSPKEAKTY PCKISYSQYSQYLSTDKLIRISA LGEEKSSPEKILVNKIITLSYPSI TINVLGAAVVNQPISQVIFSNP LSEQVEDCVLTVEGSLFKKQKQ KVFLGVLPQHQSIILETVPFK SGQRQIQANMRSNKFCDIKGY
27513	57881	A	27679	1	756	
27514	57882	A	27680	1	2601	

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27515	57883	A	27681	1	1677	MARKDLPPAYGGWQVLDATP QEMSNQVYCCGPASVRAIKEG EVDLNYDTPFVFSMVNADCMCS WLVQGGKEQKLHQDTSSVGNF ISTKSIQSDERDDITENYKYEEE HFEAFQSVAQ/LPITRPFSWILRP F*RP*RKISTSFIRPLFTFL/LRLM NAHPEFRMAMKDAKTYPGKIS YSQDSQDLSTDKLIRISALGEEK SSPEKILVNKIITLSYPSITINLLA RVLSPSLPGPAGLASRSEYGPA KPTPTGNSSWPASAAARSPGSRP CLSLHTSPQAEAGAGSLDQPRE RLPQCSGELKGSSSAARMGAE NEEAPRASEGCGGCQQA VTSQ QDGGPLLQNRFFWDCGDENGA DAVYLDSEPPRQEYVMNDYGF IYQGSKNWIRPCPNWYGQAASP WRYGQWWVFVA VMCTALGIK SCDFQAARNNEEHHTKALSSRR LFVRRGQPFTHLYFRAPVRAFL PALKKANKGKLESFSYICFFSIV FGSKNSYAKVAYLEVAYPATL QNGALRKYLVLGA AVVNQPLS IQVIFSNPLSEQVEDCVLTVEGS GLFKKQKVLIP
27516	57884	A	27682	1	1653	
27517	57885	A	27683	3	2170	
27518	57886	A	27684	2	244	ACPSTSTSHCRGATCSCSRTS/C SGVLQHSRLRHCAASGRGFSSRCP ACCGSPGLGLPAALPPAAWGL QIAPSPQGTGPNSSQS
27519	57887	A	27685	618	851	
27520	57888	A	27686	78	240	
27521	57889	A	27687	860	1246	
27522	57890	B	27688	1	2301	

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27523	57891	A	27689	1	1719	MHINTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNRREHGKKERSSPAME QSWMENDFDELREEGFRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRLSRCDQLEERR KQERSKIDTLTSQLEKELEKQEQ THSKAGRRQETKIRAELEKIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITDPTEIQTIREYYKHLA NKLLENLEMDTFLDTYTLPRLN QEEVESLNRPTTGSEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL HINRAKDKNIHIIISIDAEKAFD KIQQPFMLKTLNKLVLLEVLA IRQKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP

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27524	57892	A	27690	1	1902	MNAKALPTLSPLPQATTESVSL TQERSSSPATEQSWTENDFDEL REEGFRRSNYSSELREDIRTKGK EVENFEKNLEECITRIINTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSADEMEENEMK REGKFREKRIRKNEQSLQEIWD YVKRPNVRLIGVPESHGNGTK LENTLQDIIQENFPNLRQANIQ IQEIQRTPQRYSSRRATPRHIIVR FTKVEMKERMLRAAREKEIQ TIREYYKHLYANKLENLEEMD KFLDTYTLRLNLQEEVESLNRPI TGAGIEAIINSLPTKKIPGPDGFT AEFYQRYKEELRIKYLGIQFTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCS WVGRINIVKMAILP KVIVRFNAIPIKLPMTFFTELEK TTLKFIWNQKRARIKSLSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTEPSEI MPHIYNYLIDFKPEKNKQRGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITQIDIDMGKDFMS KTPKAMATKAKIDKWDLIK ELLTAKETTIRVNRQPTKWEKI FTTYSDDGLISRIYNEL/KQIYK KKTNNPIKKWAKDM
27525	57893	A	27691	1	2781	MGKKQNRKTGNSKKQASAPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSSELREDIQTGK EVENFEKNLEECITRIINTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMEENM DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTQORYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTLKIYAPNTGAP RFTKQVLSDLQRDL
27526	57894	B	27692	1	756	
27527	57895	B	27693	1	1743	
27528	57896	A	27694	1	1407	
27529	57897	A	27695	3	391	
27530	57898	A	27696	604	955	SSVFLGDDPILIGNKEMCLSSVL LINGSINFLHPFREDKGAVDVP GVATQQLILLNDPVLTAISELGL LVSSLSK*TSPIPGPGGNA*AR QPSCP*KGELSWRSAPSLVQFSS

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27531	57899	A	27697	1	1783	MGARAGGSCSCLMWLLASG HFMGCVAAAGDTVGPEKFRSCY TITLLQSKLSYSFGKNNKNFQL RKCLQTVDNLFVPNQNGYYCH SQTSLDRAQIDLNGRIRNGSVY SAHSTNSLNNPQPYLQSPMSS NPSITGSDVMRPDYLPISHISA VIPPSYRPTPDYETVMKQLNRG LVHAERQSHSLRNLNIGSSYAY SRPAALVYSQPEIREHAQLPSPA AAHCPFSLSYSFHSPPYPYPAE RRPVVGA VSPVELTNAQLQAQ DYPSPNIMRTQVYRPPPPYPPPR PANSTPDL SRHLYISSNPD LITR RVHHSVQTFQEDSLPVAHSLQE ERSSSPATEQSWTENDFDELRE EGFRRSNYSELREDIQTKGKEV ENFEKSLEECITRITNTEKYLKE LMELKTKARELCCECRSLRSQC DQLEERVSA MEDEMNMKRE GKFKREKRKRNEQSLQEIWDYV KRPNLR LIGVPESDGENGTKLE NTLQDIIQENFPNLAKQANVQI QEIQRTPQRYSRRATPRHIVR FTKVMKEKMLRAAREKGRVT LKG/THQT/RORISRQKLYKPEE SGGQYSTFLKKRIFNPEFHQPN
27532	57900	A	27698	3	1046	
27533	57901	A	27699	1	3585	
27534	57902	A	27700	937	1119	

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27535	57903	A	27701	1	2231	MGKKQSRKTGNSKKQASPPP KERSSPTATEQSWSENDFDLRL EEGFRRSNYSKLQEEIQTGKE VKHFEKNLDECITRITNREKCL KELMELKAKARELREECRLRS QCDQVEERTLARLIKKKREKN QIDAIKIDKGDITTNPTETQTIR EYYKHLTYTNKLENLEEMDKFL DTYTLPRNLQDDVESLNRPTTG SEIEAINHSLPTKKSPGDRFTA KFYQSLPSSCDYGHAPHPDVF RVSSFVWVRGLAGSGVKLQTF AVSVTALKAAARLELFIPPDSGA QLASPSGSLTRTGGGAACQSHA VCPHSSAFGWSMGLGAMEQG AALIGEARASREPMEVGGSG MAACRSQALPRGQLRPSEKSR APEHSSPAMEQSWMENDFDE LREEGFRRSNYSELREDIQTGK KEVENFEKNLEECITRITNTEK LKELMELKTKARELREECRLR SRCDQLEERVVSAMEDEMNEMK QEGKFREKRIKRNEQSLQEIWD YVKRPNLHLIGVPESDGENGT LENTLQDIIQENFPNLRQANIQ IQEIQRTPTQYSSRRATPRHIIVR FTKVMKEKMLRAAREKGDSV ERSFSNKAELLFQLHGHQRESL SKKEAQVWRDKGLYFRKGLLD QAQSWSRQVASILGAQIQVEGS PEQRLNVELAGGHLNLTAKAIP MVAVAGGISFKCGAVLLLGAA
27536	57904	A	27702	596	1593	KPRENLYVKNAEASGANAINW KKGY/LVMEDEMNMKQEGKF REKRLKRNEQSLQEIWDYVKR PNLRLIGVPESDGENGTLENT LQDIIQENFPNLRQATVHIREI QRTPTQRFSLRRSTPRHIVRFK ETKEKMLRAAREKEIQTIREY YKHLTYTNKLENLEMEKFLDT YTLPRNLQKEVESMKRPITSSEI EAVINILPIKRSPGPDGLTATFY QRYKEELERSSSPATEQSWMEN DFDELREEGFRRSNYSELREDI TKVKEVENFEKNLEECITRITNT EKCLKELMELKTKARELREECR SLRSRCDQLEERVVSAMEDEM

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27537	57905	A	27703	717	1803	STGRKAPHHTYSKIDHILGSKALPSKCKRT/EIITNCLSDHSAIKLELRKIKKTPQNPSTTWKLNLLNDYVWNKEMKSEIKMFFETNE NKNTTYQNLWDAFKAVCRGKFIALNAHKGKQERSKIDLTSTQLRELEKQEQTTHSKVSRQEITKIRAEPKETQKTLQKINESRSWF FERINKIDRRLARLIKKKREKNQRDAIKNDEGDITDPTETIQTIR EYYKHLAYANKLENLKEMDKFLNTYTLPRLNQEEAESLNRIAGS EIVAIHNSLPTKKSPGPDGFTAIFYQRYKEKLVFGAGYFGMWAL AALPSNLLKLSQLCQEAEEVNV LVQFVCICPAQEPTIDVLFVSL PPLSLILN
27538	57906	A	27704	407	1696	NILRNAVPHQQONKA*RRMTLTS*EKKASDDQTPSYRRKFKA KAKKLNT/YEKNLDECITRITNREKCLKELMELKAKARELREEC RSLRSQCDRLSEERVSVMEDEM NEMKREGKPREKGIKREQSL QEIWYVYKRPNLHLIGVPESDR ENGTKLENTLQDIQENFPNLAR QANIQIQEIQRMPQRYSSRRATP RHHIVRYTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLLAET LQARREWGPFIKILKEKNFQPRI SYDPDKLRFISEGEIKYFTDKQML RDFVTPRALIEALKEVLNMER NNRSPSSSPATEQSWMENDFDE LREEGFRRSNYSELREDIQTKEG KEVENFEKNLEECITRITNTEKC LKELMELKAKARELREECRLSR SRCDQLEERVSAEMEDEMNEK REGKFREKNKKK
27539	57907	A	27705	2597	5904	
27540	57908	A	27706	1	675	
27541	57909	C	27707	137	1357	
27542	57910	A	27708	1	1032	

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27543	57911	A	27709	3	959	MANNPGANGQIPGGPGGPGMG KPRCF/RGEVFGIVIRGRGSRP/R GRGRGR/GRGARGSKGRG*RE WNAVHVQVGAALVKDH*RSKFP WKEIYLFSLPH*RNQRIIDFVFLG GLLSKDEGFE*LCPVQKQTRA\ GQPHPGFKAIFVAIGDYNGHV GLGVKCSKEIVATGHPVPGAINL AKLSIRPRCAEGYLGKVLAKP VHTVPLQGDGKRGCGSVLVRLH PLHPRGTGIVSAPVA\KKLLM MAIGIDDCYTLS/ARGCTATLG QIWPRATFDAISKTYKLP*PPD LWKETVFTKVAPYQIEFTDHLV KDPHPRESSVQDSELQLVATT
27544	57912	B	27710	50	1598	
27545	57913	A	27711	1	3916	
27546	57914	A	27712	334	462	PAFITYNKCSSARKLIQV*GPVA CRVHILPLVVRCPKPGTTG
27547	57915	A	27713	256	654	
27548	57916	A	27714	1	855	
27549	57917	A	27715	211	436	
27550	57918	A	27716	19	319	
27551	57919	A	27717	987	1392	RHCLCSPSRSSSELQPTASSSSA RSSPSPASQVPPGPAGAAAAAP HPPCCPPESTCWTWPC*SPLCH WAVA*ARSGPGLGECFETHGP HGCPGQSPRPQ*APSAWWTE VQPR*PRPAEGSSRRPPPGAP
27552	57920	A	27718	285	1266	RSQIQRGTDRAKCTSGPPHVRV AQODDAPREPPYLPNGMPFG RDAPHLDPWAASQRGSSHPRR WPPSQRRSLLPRRVADRPEAAI SALWEAKAGGWETLPEMEITH NKTRQSKRITHQTNRPNTSSKTI RITKTDLTSWETQSPGSPDRHR KPSTATKHNRFSKIYSRFSIFQC DQGLNGRCGQKGAGKEQRM QEQQENFQAPPFQSHPALRSLQ MQQVQTEEHFGTLECGKLAQC SFHPTREEDRNQDGKTDMLHF KLELPLQSTEHVLGVQLITFSY RLHSCGIPSVLSRYPYFMSLAFG ILSRTLRRFVTVSSLLITGI
27553	57921	A	27719	1518	1779	ARSGPGLGECFETHGPHGCPP GQSPRPQ*APSAWWTEVQPR* PRPAEGSSRRPPPGAPCPAQP PTRRCFGRHQTPAAGAAVP
27554	57922	A	27720	507	1114	
27555	57923	C	27721	80	223	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27556	57924	A	27722	1	2373	
27557	57925	A	27723	2	272	RARTPLWPRARGPGSRVSGAP WFLLDLAGGGLPPAVLCDLSA ASSTVSGRSNPHC*AWGGLLEFF GEVERAESGFPVPEPSLISEMPH
27558	57926	A	27724	195	489	
27559	57927	A	27725	210	1308	
27560	57928	A	27726	203	474	
27561	57929	A	27727	224	892	
27562	57930	A	27728	1	457	
27563	57931	A	27729	3	1325	
27564	57932	A	27730	322	512	
27565	57933	A	27731	621	737	
27566	57934	A	27732	441	588	
27567	57935	A	27733	1	792	
27568	57936	A	27734	8	488	SGCRNSARADADPSLHASPPAP TMA TVQLLEGRWRLVDSKGF DEYMKELVGVGIALRKMGAAMP KPDCHITCDGKNLTAKTESTLK TTQFSCITLGEKFEETADGRKT QTVCNFTD GALVQH QEWGDK ESTITRKLKDGKL VVECVMN VTCTRIYEKVE
27569	57937	A	27735	861	2161	
27570	57938	A	27736	349	625	
27571	57939	A	27737	1	630	MAQETNHSQVPMCLSTGCGFY GNPRTNGMCSVCYKEHLQRQN SSNGRISPPATSVSSLSLPVQC TDGSPVEAQSALDSTSSMQPS PCIKQSLLESVASSQLDSTSV KAVPETEDVQASVSDTAQQPSE EQSKSLEKPKQKNRCFCMRK KVGLTGFECCGNGVSCSHRY SDVHNCSSNYKADAAEEN/LE KENPVVVGKIQKI
27572	57940	A	27738	1	1089	
27573	57941	A	27739	41	334	AGKMTKLEEHLLEGIVNISPO*S VRKGHFDTLKGLKQLLTKE LANTIKNIKDKAVIDEIF/QGLD ANQDEQVDFQEFIS/LVAIALK AAHYHTHKE
27574	57942	A	27740	1	519	
27575	57943	A	27741	28	314	
27576	57944	A	27742	208	421	
27577	57945	A	27743	619	890	
27578	57946	A	27744	113	328	LGSGAWGGDLPEWENPLSSCS LLREKDLLTTS GPQT VTS PRNISP ILNRDPTVQLTWQPLPEPELW PKAL
27579	57947	A	27745	501	680	

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27580	57948	A	27746	166	405	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQPRNISPISNRD PTGKWTVQLTRQPLPEPELWLP KALRLTPSQIFSA
27581	57949	A	27747	425	484	
27582	57950	A	27748	448	520	
27583	57951	A	27749	3	679	GGGFSRDRDTALQPQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGKFFYPKAMG AMEGSGQRRLTDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFCAVT RIGGLPWVFNPLSSCLLREKD PPTTSGPQTVTSRNISPILNPELA TLAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP EPELWPKAL
27584	57952	A	27750	3618	3848	NLCCKEPSSRRSIHKESLLNFPLM GLDPRPQEGFPRDSPR*REESTS LHDPMASSSTVFWGLKRQKY FLWPFRAST
27585	57953	A	27751	1	297	
27586	57954	A	27752	244	420	RKETKERSRTPP*SPRTGQMTP CKLQPGVLSFPRTAQSWEPAPV PQSPLKNELRRKYLT
27587	57955	A	27753	1993	2205	
27588	57956	A	27754	138	833	
27589	57957	A	27755	1	875	
27590	57958	A	27756	1	1041	
27591	57959	A	27757	3	1447	
27592	57960	A	27758	23	3257	
27593	57961	A	27759	2	168	GKAGCWPRSRARKCRTCSPSIW AAWRPPTR*LTVTSRPGTSGSE PWMAAASRWQ
27594	57962	A	27760	85	1271	
27595	57963	A	27761	5871	6056	TSSAASTAPRWRKPHGHQKSL PASLRFPGR*TPQDLPGPAPQ PAQPGPPQAATVPGRW
27596	57964	A	27762	1	280	
27597	57965	A	27763	1	714	
27598	57966	A	27764	2	558	RRAHACARRRRKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLLAMVNPMTFFH IADVGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFGYKGSFCH RIIPGFTCSQSGDFTRHT/GIGGKS ICREKFDCKNFILKHTGPGLISM ANAGPSVNV

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27599	57967	A	27765	1	927	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSVFVRGLD TKK*LLI*SIKLC*QIGSSSIFTS D*KNSCLPLIVQQCLFLRLPL FADKVPKTAENFRALSTGEKGF GL*GVPCFHR/IIPGFM/CQGGD FTPP*MAPGGKSIYGK/FEDEN FNLKHTGPGILS/MANAGPNTN GSQFFICTAKTEWLDGKPVVF GK/VKKGLNIVEAMERFGSRNG KTSKKITADCGQLISFDLCFIL NHQDHSFCALLSGEHPSTPFAR RILRILWLSQLFLWGSMSFLFPP MPSWIAAVKFMIIKTK
27600	57968	A	27766	1	798	
27601	57969	A	27767	1	575	PTRPPTRPPTRPIMAQDQGEKE NPMRELRIKRLCLNICVGESGD RLTRAAKVLEQLTGQTPVFSKA IRYTVRSFGIRRNEKIAVHCTVR GAKAEIELEKGLKVREYELRKN NFSDTGNFGFMQDHIDLGIY DPSIGIYGLDFVYVVLGRPGFSIA DKKRRTGCGIAKHRSKEEAMR WFQKQYDGILPGK
27602	57970	A	27768	1	1695	
27603	57971	A	27769	1	228	
27604	57972	A	27770	1098	1938	IWPRPRDC/RVSYTTVFPPATVT APV/VSGGSHDHIQQYSDIEDFR QATAASSVMVARAAMWNPSIF LKEGLRPLEEVMQKYIRYGGM GAALLSDPDKIEKAPSMGTL GVYLPCLQNIQFVILFLRLTWM VGTAGVLQALLIVLICCCCTLL TAISMSAIATNGVVPGYLHTLV QNLVNNGYVRDETURAAPYD WRLEPGQQEEYRKLGLVVEE MHAAYGKPVFLIGHSLGCLHLL YFLLRQPAWKDRFIDGFISLG APWGGSIKPMLVLASGSGTRA
27605	57973	A	27771	1	1710	
27606	57974	A	27772	163	1659	
27607	57975	A	27773	3	297	
27608	57976	A	27774	3	447	SSPHSSRSLSAPPLPGLPLWRHL RSPSAHRCTVGAPFWAGEGRSP LPQLAGRCGGRASGNRGARG ACGPAGVPGGRGLGGPALGAA GRPGP*LPSRGAAGLTA/GPPCL SLPPPPWVPVQPEPPRRAPPAP RRPVPSAQGLRSASA

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27609	57977	A	27775	3	197	RPDVAPARSLEMKRFMPMPPPP G*FSPGASLDVNP GCYKQAPSC SLAQILSNLSNLWSSAVSNF
27610	57978	A	27776	77	379	GRLLDKAGIPH/PPFPSSGLGCQ H*RRSPLHEHPSSGP/PAGLKPS LSCLPAGQGS GPAARY/GLSLPP TPWAPVQPEPPRRAPPA PGRS VPSTTQGLRSASA
27611	57979	A	27777	177	444	RGGQGS GPAACYA*/RLPTPW APVRPEPPQRA PPPAPRRPV PST TQGLRSASTRRVTGRQLHLQP WCGIHWVKPAGLLSLVGRWRV LMS
27612	57980	A	27778	165	591	QRAQSPHSPRSL SAPPLPGLFLW RHLRSPSAHRCTVRAPFWAGQ GRSRLPQLAGRCGGRGASGNP GSHGACGPAGVPGGRGLGGPR TGSSQLALPAGNEGLSTP ASG RRKKLRTHPSIRRNKLQTRYLK SCNTHREGPRLH
27613	57981	A	27779	1	1605	
27614	57982	A	27780	2	1970	
27615	57983	A	27781	1	3522	
27616	57984	C	27782	183	254	
27617	57985	A	27783	39	346	QYISELQFLASTVRQTPATSPA H KNFQTPEPQQGPPEPPPPGAC YKCWKS GHQAKECLQFGIPRK/ HASHLWQPLPEPPGT LAQGS LT DSFPDLLGLAAED
27618	57986	A	27784	1	354	
27619	57987	A	27785	72	299	
27620	57988	A	27786	273	530	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQKEHLTNFKSG PH*KSDCSTAPGATPRAGT LA QGALTDSFPDLLSLAAED
27621	57989	A	27790	1	1068	
27622	57990	A	27791	148	527	
27623	57991	A	27792	2	1910	
27624	57992	A	27793	1	1047	
27625	57993	A	27794	96	488	WDRMAGSSNTFGFPPLPYR SCER*QRDGGPRSPGSLVPPW PR/PPILAALEEPSPLHRRGRPS LGWPRPELAPSAQRSAAS/RPEA SKDHEPTRKKE/TPDTQP*EL* HSLPRSSASLALGPHYLYEL
27626	57994	A	27795	3	2086	
27627	57995	A	27796	3	412	
27628	57996	A	27797	2	390	

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27629	57997	A	27798	1	629	MKVGLDQHIEVVPVSHSVTSGLAA AGECGGVHCDSDVCAEGRWGP CSLPCYCKNGASCSPDDGICEC APGFRGTTCQRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNE/RLFTVCPSPGR FGKNCAGICTCTNNGTCNPIDR SCQCYPGWIGSDCSQPHCADKC VHGRCIAPNTQCCEPGWGGTIN CSSVKKQSTVCES
27630	57998	A	27799	108	1071	YPLFLSSISACDGDHWGPCHTS RCQCKNGALCNIPITGACHCAA GFRGWRCEDRCEQGTGNDCH QRCQCNQATCDHVTGECRCP PGYTGAFCEDLCPGKHGPQCE QRCPCQNGGVCHHVTGECSCP SGWMLSPFGWRPI*FSKSL*MQ GTVCGQPCPEGRFGKNCSEQC CHNGGTCDAAATGQCHCSPGYT GERAAVPDVRKCCQDECPVGYT GVLCAETCQCVNNGKCYHVS ACLCEAGFAGERCEARLCPPEL YGIKCDKRCPCHELENTHSILIA AKKSNSLHAIALDFRAQCQSVK DRCHASDLPIDIVSTETLR
27631	57999	A	27800	243	1296	ETQEESSFEPLCGSHQPNQ*LLF CSTYKRCLCNWGPC*AY*RACP CPALQQCPDI/CPQAQLAIPCAP QQQQLSRCLSPFSSLLQDPNTP G/EYRKDEGRAGSRGAGEKQC THNSPRWLQNTVSNQSSMPG FQSHVPSLLGAFVQCTNCTRV SSPANKIFTTFLRGDPLVSPCHQ GFGSNTHCCVESWQSSCSGMH KDLGALHTPAPGSPTNVAATQ ARREPRCLAVLSTLDRSTRQK VNKDIOELNSALHQADLTDIYR TLHPKSTEYTFSEPHRTYSKTD HLVGSKGLLSKCKRTEHTNCLS DHSAILKLELRKKLTQNCSTTW KLNNLLNDYWVHNEMKAEID
27632	58000	A	27801	552	827	
27633	58001	A	27802	70	200	
27634	58002	A	27803	18	1057	
27635	58003	A	27804	652	960	
27636	58004	A	27805	1	474	
27637	58005	A	27806	1	140	
27638	58006	A	27807	1	1260	

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27639	58007	A	27808	126	893	EDGSGGGKFPEGARQGGTGQR RRRKAMRRGTGAPAQADSRGRG RARGGCPGGEATLSQPPRGGT RGQEPQMKETIMNQEKTTHTC RHKVRIGGKGTARKKKKVHH TATA/DDKKLQFLKGS*GVN NISGIE/VNMFNTNPRNKLHIF*Q PLKVQGISWAANTFHHLQGH *DKSSWTEMLPSIFKPSLGAG*V *LVLRRLA/EALPQTNLWDGKS TTLLEDGDDGDDDESSQLWEY FGWRVPRNEANLNLSTF
27640	58008	A	27809	180	589	KELPLLIFCRWQFESLHNLNVPF FKVSGDGTNNFPYLEKTAKKG SPNGDLPGCKSNHGP*SKFIRS VKPLNPQLLASLQCTSAAYPLQP EDVNLRVISVSRREGVFPFLGHL LWGRRLSFYNQNSNKHGILYN
27641	58009	A	27810	623	1082	
27642	58010	A	27811	548	645	
27643	58011	A	27812	329	510	
27644	58012	A	27813	3254	3628	
27645	58013	A	27814	1	960	
27646	58014	A	27815	349	681	PMASNRAITLTAWPKIPFLGICE AKNPRSENML/AHHFGSLPP SWELWEQPPGNSSRYIEFLNK HTYIKGTLRVYTKKFCMLVIKS FESKSCVWRYDFDSKSSVNVTV
27647	58015	A	27816	240	473	
27648	58016	A	27817	825	1043	
27649	58017	A	27818	2	418	GKVVCFEAFLOQLGKHQFYW CLEGLGHCHHHIGAKYPEDIVD EESAQQDAASADIVEVQELYSI KGEQAKKVVGPNVLPQQVPD ANDAAQAQAHQVLGVKFHDD L*AERPCKSTP*GRATPPTFLVF PRTLCEGI
27650	58018	A	27819	2	427	
27651	58019	B	27820	51	672	
27652	58020	A	27821	43	667	
27653	58021	A	27822	516	1056	WSRAPAPQQCQHWLHPAGRTL HLRCLLGIWHQCDGDSGQVLR GTNENLVFPQDLLEKGLEANNF AMLGTWEMSSFPGIFIALLLRF DISLKKNTHTYFYTSFAAYIFGL GLTIFIMHIFKHAQL*GVKS*GS SGSDRIQRGNRGISIEGA GEERE MMQLVPEPLRARPDWGLGPH RRA
27654	58022	A	27823	1	1019	
27655	58023	A	27824	1061	1258	

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27656	58024	A	27825	44	621	
27657	58025	A	27826	406	727	
27658	58026	A	27827	2	1337	
27659	58027	A	27828	1236	1391	
27660	58028	A	27829	228	502	
27661	58029	A	27830	1	1035	
27662	58030	A	27831	146	392	GHRSHQSP EETPNLIPRTPIPLPG TGTSIRSTRIPRTEASGPNGLN WYLTPTPPGGQRPSSAASPRGF PPTNNSRLPAEPE
27663	58031	A	27832	15	300	
27664	58032	C	27833	289	414	
27665	58033	A	27834	3	576	AALAERWLGEVLVRVGVVRVPG GSGGLRHWCPGGLLRGLGQA PEHKVRLSMEFCSTCTADHISLS SFWRSSFQQPLVPAVSLQSPDR RLSHDPAASSWSGFCGISPAFSA FSECPSSSLRSHPPALLQAAES* FAASSPSPPTWSLGSSTGRKPW S/VACNWLLSDSSSHRSPFWS GHITMVLALTLEELV
27666	58034	A	27835	1	231	DELLVGGNPRGDAEEGRCP GGVGVRVYQIQIWPRLCSRNP GAAD*GPGS*RWDRCPRDEIWR FLGALVGSVSSG
27667	58035	A	27836	18	398	KVRWERSWSESESESEQGRRR AQALVPSVAS*/SSRPWDRPST K*GCLWSSAARAQQTIYHSVPS GGHPSSSHWLPAVSLQSPDRRL SHDPAASSWSGFCGISPAFSAFS ECPSSSLRSHPPALGSF
27668	58036	A	27837	1059	1446	AVWSLPAPAPCLLAGLLTCC RTP*TASLCARGVPRPRA*EAT RGTS*A*ALHSPPGTLPTVTRTS PSHLSARAAAAPSHPARPTASRSS RLPAWLAVRLSIPPRRGLGGA GAQAAAATRFTCCS
27669	58037	A	27838	1	211	ATAAERWLGEVLVRVGVVRV CGEWRAQALVPIVAS*ATRPSG RGPTTQQT*RTSRIGRS*QTMR HART
27670	58038	A	27839	316	537	
27671	58039	A	27840	255	475	RPWVRAPYKLLPALLHAPLCAP PSSPWRPV/PASAPSKLLKS*IF CKQLSLPTWSLGSSTGRKPWS GPVTGS
27672	58040	A	27841	622	1127	
27673	58041	A	27842	364	666	

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27674	58042	A	27843	37	299	ILLCSVQTLPLLRREFYGHIPKC QQSLNIICSPSLRIPGFLHRNRL STPFHVQQPQREHF*YCRSQIH GENSAWHIRSHHAKEKAHF
27675	58043	A	27844	84	428	PAEIERSTAKTPGPPGSLEMGLL TFRDVAIEFSLSEEWQCLDTAQR NLYKNVILENYRNLVFLGIAVS KQDLITCLEQEKEPLTVKRHEM VNEPTGPRQKRRVTSSR**MKR YVII
27676	58044	A	27845	1	719	
27677	58045	A	27846	669	830	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLLHPNDQQAAPVWT ENQPGGHW
27678	58046	A	27847	223	382	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLLHPNDQQAAPVWT ENQPGGHW
27679	58047	B	27848	1	491	
27680	58048	A	27849	1	1113	
27681	58049	A	27850	505	1105	ITCTLYPSLRIVYEAFPATGDNM FRRIJKDALFRTIQFCQIMNRSQ YMFTCRCRTEMQVPQHRKKKT FKFTVLLNHFMVIEIIVLTAGRID AAFDQDEVAASEGFLKQPVGKD YKFGGSPVKDEKLFVGVTGMG HHN*LSV*TSIQHLLSNTQG/CL RVCAPALRL/HSRNLAMVISFSF SCGARSAISPINAKRWASPVC
27682	58050	A	27851	1	2697	
27683	58051	A	27852	1	1998	
27684	58052	A	27853	864	1025	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLLHPNDQQAAPVWT ENQPGGHW
27685	58053	A	27854	1605	1766	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLLHPNDQQAAPVWT ENQPGGHW
27686	58054	A	27855	677	735	
27687	58055	A	27856	1126	1568	SSSTGRSRHKEVSPGCQDGL RCQEWWSVRPGYEATGGVWG KQLGIPASGLPGRSSSPRKSC TPVTSRTGLPVCWAALESER SFSLSVRPVVCVCGTKMSCA PECCFFLYSLSLSLFLRLLLGL AAHCQFFPAVPLCIL
27688	58056	A	27857	1142	2450	
27689	58057	A	27858	1	1131	
27690	58058	A	27859	229	402	
27691	58059	A	27860	505	597	
27692	58060	A	27861	1	657	
27693	58061	A	27862	248	382	QPPKITLLYQQWIQTKKSLKS FLP*QEFRMKQKHKSTKSSITL

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27694	58062	A	27863	1	1341	
27695	58063	A	27864	1	739	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRKIKLTQNHSTTQQLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWYVKDTRI SGMLWYVKA VCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKTSRRQEITKIRAELEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKREKNQIDAIGN DKGDIITDPTEIQTITREYYKHL YGNKLENL*H*MPTRESRKDLK LTP*HHN*KN*RSKSKHIQKLAE GKK*LRSEQN*RK*RHKKPFKK SMNAGAGFLKRSTKLIDR
27696	58064	A	27865	1	1920	
27697	58065	A	27866	444	763	
27698	58066	A	27867	1	651	
27699	58067	A	27868	94	964	VNADWVLQRELEQTSWSSKQ RACCLSHVVGLRMISSCTTRKM AEEEQRKIPLVENLLKKRKA Y QALKATQAKQALFGKEGAEER KRAQ/WFKRLESFLHDSLAAET *QG/RISRQLEVQPHALELPDKC SLAFVVRIRKIDGSGLLVQRTIA RLCLKKIFSGVFVKAPPRIQKW LRIVEPYVTWGFNPKSVRELIL KRGQAKVKNKTIPLTDITVME EHLGKFGVICLEDLIHEIAFPKG HFQEISWVLRPFHLSVAHHATK NRVGFLEKMGTLGYRGERINQ LIRQLN
27700	58068	A	27869	176	334	
27701	58069	A	27870	3	452	AASTGGGSHLLSIMALRPLV KPKIVKKRTKKFIRHQSDRYVK IKRNWRKPRGIDNRVRRRFKQ ILMPNIGYGSNKKTKHMLPSGF RKFLVHNVKELEVLLMCNKS YCAEIAHNVSNNRKAIVERA VQLAIRVTNPNARLRSEENE
27702	58070	A	27871	2	423	
27703	58071	B	27872	193	1698	

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27704	58072	A	27873	263	714	KLNVPPIKATNTIMNMTMNLK MSLTAPPSDICRGPKLSFAGKIQ AIEPEKLKTTATAQRPLDTIGLEV PVPAAWLLSAVRNCSKLRATS GPNLDTMNGSRRTGSGWTEGS RSSMKPHLLSDITGALR/SPKVS *AFCRLATWPFNLFQSGILS
27705	58073	A	27874	347	902	
27706	58074	A	27875	17	1178	
27707	58075	A	27876	1	1155	
27708	58076	A	27877	3	1109	EKETMQSLNDRLASVLDVRVS LETENRRLESKIREHLEKKGPQ VRDWSHYFKIIEDLRAQIFANT VDNARIVLQIDNARLAADDFRV KYETELAMRQSVENDIHGLRK VIDDTNITRLQLETEIEA/LKEEL LFMKKNHEE/EVKGKLTPTYA ALG*TVVEVDAPKQSDLAKI/M ADIRVAQ/YDELGSERTEKLDK YWSQIEESTTVFTTQSA/EVGA AETNLHRSCLKRTV/QSLEDPRW TSMRNLKAQLGEQP*GEVEAPL RPTRWSQLNGILLHLES/ELAQT /RAEGQRQA/QEYEALLNIKVKL /EAELATYRRLLEDGEDFN/LGD ALDSSNSMQTIQKTTTRIVDG KVVSETNDTKVLEALSQQKAG
27709	58077	A	27878	1	1305	
27710	58078	A	27879	209	560	
27711	58079	A	27880	219	512	
27712	58080	A	27881	528	803	
27713	58081	A	27882	3	432	SSPCVEFSTSMGACLRPATARS SATCTAWTCTGWRGRPWWR WTPENSGVAGGDTSEEDSEE VEGAEWGRRRRQRRGERCG GLRRAPCQGAPGKCLCPRP/PGP SPC*/CEALGAQRAS*PHRELK VGGPGPGCELSPMV
27714	58082	A	27883	117	483	
27715	58083	A	27884	1	1497	
27716	58084	A	27885	228	776	
27717	58085	A	27886	1012	1677	
27718	58086	A	27887	194	562	
27719	58087	A	27888	1	423	
27720	58088	A	27889	232	308	
27721	58089	A	27890	1	1692	
27722	58090	A	27891	186	2191	
27723	58091	A	27892	2	141	
27724	58092	A	27893	1	1692	

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27725	58093	A	27894	186	2192	QRRPRPFPSQGISMTECFLPPTSS PSEHRRVEHSGSLTRTPSSEIS PTKFPGLVYRTGEPSPPHDLHEP PDVVSDDEKDHGKKKGKFKKK EKRTGYAAAFQEDSSGDEAESP SKMKRSKGHVFKKPSFSKKKE KDFKIKEKPKEEKHKEEKHKEE KHKEKSKDLTAADVVKQWK EKKKKKKPIQEPVPQIDVPNL KPIFGIPLADAVERTMMYDGIR LPAVFRECIDYVEKYGMKCEGI YRVSGIKSKVDELKAAAYDREES TNLEDYEPNTVASLLKQYLRLD PENLLTKELMPRFEEACGRTE TEKVQEFQRLKELPECNLLIS WLIVHMDHVIKLETKMNIQ NISIVLSPTVQISNRVLYVFFTH VQELFGNVVLKQVMKPLRWSN MATMPTLPETQAGIKEIRKQE FLNLCLHRDLQGGIKDLSKEER LWEVQRILTALKRKLREAKRQ ECETKIAQEIASLSKEDVSK EEM NENEEVINILLAQENELTQEE LLAMEQFLRRQIASEKKEIERLR AEIAEIQRQHQHGRSEETEEYSSE SESESEDEELQIILEDLQRQNE ELEIKNNHLNQAHEEREAIIE RVQLRLLMQRAKAEQQAQE DEEPEWRGGAVQPPRDGVLEP KAAKEQPKAGKEPAKPSPSRDR
27726	58094	A	27895	12	413	PSRAPGLQKACTGHGEMAVHP PRIPVQSDHLISIEGLLCKLP GQVTKESGLVSFSLRPVLPQNT LSNSFYLFPGYASPYVETFLPG AHSGPAPPLPVRTPTAKRL/G VAVAPSPTF*ISPRALRSTFVSN
27727	58095	A	27896	1	361	
27728	58096	A	27897	2	162	
27729	58097	A	27898	248	381	
27730	58098	A	27899	73	254	
27731	58099	A	27900	1	729	
27732	58100	A	27901	1	762	
27733	58101	A	27902	2	334	
27734	58102	A	27903	3	369	
27735	58103	A	27904	669	1006	
27736	58104	A	27905	3	250	
27737	58105	A	27906	721	876	
27738	58106	A	27907	3887	4013	
27739	58107	A	27908	3423	3627	

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27740	58108	A	27909	3	226	HETGCCGQAAERDSCWERPPIP LLLPSLSGDYETVRNGGLIFAG LAFIVGLVILLSRRFRFCGGTKKR RRINEDEP
27741	58109	A	27910	67	264	
27742	58110	A	27911	161	851	
27743	58111	A	27912	139	351	GGRRIETGGWERPPILLPSLS GDYETVRINGGLIFAGLAFIVG LLILL\SRRFRCGGNKKRRQINE
27744	58112	A	27913	2	431	
27745	58113	A	27914	217	289	
27746	58114	A	27915	255	389	KPNACSHS*VGTEQ*EHMDTG RGTSHTGACREALDRGPAWEK L
27747	58115	A	27916	14	460	NCLTRRRRRRRRTFLEERLKP SRKKITKKHTKKRTASLILHAM ICCRSLNSSKTKNTKCLNSINQR LKILSLQKDL\CGTAGRCKTLT EQ*LNNTAII\CLLLREARKTL MTHQSTWTWMKLETIILSKLTQ EQKTKQRMFSLISGS
27748	58116	A	27917	503	1046	
27749	58117	A	27918	3	198	
27750	58118	A	27919	54	320	
27751	58119	A	27920	443	477	
27752	58120	A	27921	1	963	
27753	58121	A	27922	1	2292	
27754	58122	A	27923	3	736	SCCLHSRLVRARRLRRAVAVM AAQCVR\ARRSLPALASVRPI FPGL\CTATK\QRTSAKNLKG MGQSEQRADPPATEKTL\EEK VK\LEEQ\KETV\EKYKRALAID TEELTGRGSQNLLREAKLLRHF KPFCKDLLEVADVLEKATQCV PK\EEIKDDNPHLKNPLWRGLV MTEVQIQKVFTKHGLLKNPV GAKFDPYEHEALFHTPVGEKEP GTVALVSKVG\YKLHGRTLRP ALVGVVKEA
27755	58123	A	27924	253	363	
27756	58124	A	27925	235	318	
27757	58125	A	27926	1	426	
27758	58126	A	27927	146	254	
27759	58127	A	27928	1	1401	
27760	58128	A	27929	61	457	LESTLATAERFLIPSPSTGN*L VCFCTT*GQECYSVTRFSLGYG SPGCLYA*SSLIPCWRWGTPRL CCEKPFTHFCLRFVSPSKLAVS RWHIPLGSEKRRSMSAGTISL HFIWMKSPTRTSFQHFCT
27761	58129	A	27930	1	567	

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27762	58130	A	27931	128	586	
27763	58131	A	27932	271	465	HLTRPGTLLRQNFQRNDQAAT LAVHQYPLLCNSRC/CIPRQT/W VWSGPPANSNRPAEAGPDC*KE N
27764	58132	A	27933	1	375	MQKSPICVAHAGSCLLEFLF GHLGGHHDPDKPRDTRKDN FRPISLMNIDAKILNKILANRIQ QHIKKLIHRDQVGFISGVQGW NIRKSINVIQHINRTKDNHMI SIDAEKAFDKIQGFMLKILNK LGIDGMYLKIIARIYDKPTAKIIL NGQKLEVFPLKTGTQRCPCLSP LLFNIELEVLARAIQKEIKGI QLGKEEVKLSLFAHDMIVYLEN PIVSPQNLLKLISNFSKVSQYKI NVQNSQAFLYSNRQT*AIAGA PPASLPCCSLISDCCASNE*GSV GIGPSKPGAGYNLLCHLISPSIS PTSSPKSDTCPIADFSNKSPPDRSS AGDILLAMQSLGSMIAFTILILP THEHGMFFHLFVSSFISLSSGL
27765	58133	A	27934	1	1059	
27766	58134	A	27935	1	533	LSKQGHNLQRFLLPFGIC*CLP LRGGVYVRGRQASLSCGGLHP V*ASIRQLCLPTQALAMAGTPP PASLPCCSLISDCCASNERGSGV MGPSEPRCGNNNLVVC/RFLSL SEKRSSIRVGVTRFS/RCHLSQL CLATKGNLTPCTSQVRRCLTL LQLTLGAMQPLSCGLPTLSDKP
27767	58135	A	27936	140	426	
27768	58136	A	27937	1	918	
27769	58137	A	27938	54	102	
27770	58138	C	27939	244	462	
27771	58139	A	27940	234	282	
27772	58140	A	27941	328	1212	
27773	58141	B	27942	245	338	
27774	58142	A	27943	483	635	
27775	58143	A	27944	9882	10134	
27776	58144	A	27945	2	370	
27777	58145	A	27946	1682	1945	
27778	58146	A	27947	1172	1732	ESTAAEADTRFGCSWAVWAVE AEGEDCCCCCCCCCCCCCCCC CCCCCCCCCCCCCLPPSAGGRGP SGSARYFALIDAAQREDGGDA YRVGLAAALEVNAAETVACGG LEGGEAPTDAGTRYVYLEPAAPQ LSVLWKRVEVQRLVPVRVVVA AWHAARKARWLRRRAARPGP PASCALRRPSGYAAARN

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27779	58147	A	27948	272	393	
27780	58148	A	27949	333	622	
27781	58149	A	27950	11	1850	
27782	58150	A	27951	1	1107	
27783	58151	A	27952	1	1348	
27784	58152	A	27953	3	431	KLQNEILLHLVSHPGHADAKG GFPWP*AAPPLWLCRVQPSFWL LSWAGIEGLWLFHTHDTSCQWI YHSGVALADVI.HESPAIQOTS VWTSRSFHTSSEIQAEVPPKQLL TSVHAQAQYSMEAPKAWGLYP LKPWPELYLGP
27785	58153	A	27954	364	1117	EGHRAEGQCTGSVVLLTSSIGR SGKQSSGCHFWLLQHICITCPS RVMGPRKKHRTARGSRPPQPL PSGFPSAGAMGQVHCLAAPHS LERVRNPRQTQ/PPG WEG/PPTR ANLALLPTPAATATNSSIPDSP PGSDGSVPAGLTTWLAVLTLD CPKAFGKVASQACLLWKGEQP PKTPPVTPSRVSLLASEPNTIRL KNVFPFRVPACTWKSHRHSTPA HESSQKGLYPAPKPGWSCPRL WEPTSCISVTWM
27786	58154	A	27955	1	224	QWRHCNRSLLPVQKSGALEG IGPPRVFPPE*RAFGGQRAAPPDI PPPSPRHPTKDRRTAARSGPRR KRGQTNE
27787	58155	A	27956	681	879	LQISHPGHADASGGFPWPWAA PPLWLCRVQSPS*LLSQPGVECP QLFQAHSASRHLNMRPQMNS S
27788	58156	A	27957	835	1482	
27789	58157	A	27959	1	522	
27790	58158	A	27960	2	396	
27791	58159	A	27961	1	1501	
27792	58160	A	27962	473	860	
27793	58161	A	27963	370	3675	
27794	58162	A	27964	52	117	
27795	58163	A	27965	3	290	PRKTQVFGGTVEVLLKYKTG ETNDFELKNQLLDPARD/DQII NWLLEFRSSVMYLTK/DFE/QLI SIILRLPWLNRSQ/TVVEEYLAF LGNLVSA
27796	58164	A	27966	1	2988	
27797	58165	A	27967	1	666	
27798	58166	A	27968	274	930	
27799	58167	C	27969	13	231	
27800	58168	A	27970	46	386	
27801	58169	A	27971	3	451	
27802	58170	A	27972	160	494	

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27803	58171	A	27973	1	2406	
27804	58172	A	27974	201	1069	
27805	58173	A	27975	450	647	
27806	58174	A	27976	329	697	
27807	58175	A	27977	141	1506	
27808	58176	A	27978	1	1773	
27809	58177	A	27979	3	460	PHRVMGVPISRGTLSVFF*PS* CTTWPGSLGSCCTTACQVRCQPQ APHQP*APPERTTSAPAAQSPSR SSLWVTAPLVASCTCSPATHP TRSQMPSTHTPCCRGSPPRGRS PSWTRTWITCPKASKADPKAP WPCSLMPFYAQQTGLGET
27810	58178	A	27980	1	1803	MGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRYNRE PTKWEKIFTTYSDDKGLISRIYN VLKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKKHMKKCS SLAIGEMQIKTTKKMLLYYDVI RICHDSHKELEQKLAFLGMED AILYSSCFDANGGLFETLLGAE DAIISDALNHAISIDGVRCLKAK RYYRYANNMDELEAAYRRSTR PLSTRLFSFRSRVLTFRVCPCL VHTTWGGNLMRLSARSLWQR AAVNIPKLEGIIEEY/ALLV/WR AML/TEVNLSPNGLVDRINFG AHKDMALEDFHRSAIAIQGWL PRFIEFGACSAEMAPEAVLHGL RPIGMACEGDMFRATAGVNTH KGSIFSGLLCAAIIGRLQLNQ VTPTTVCSTAASFRCGLTDREL RTNNSQLTAGQRLYQQLGLTG ARGEAEAGYPLVINHALPHYL LLDQGLDPELALLDTLLLMAL NGDTNVASRGEGGLRWLQRE AQTLKQGGIRTPADLDYLRFQ DRDTSQGSRRVDCSVWELCRA GRTAGVMAVAAKTKNAGKWH NHIIRFDINPGDRLYDQGGRA HHPFAGTHHQYYRHRSRR
27811	58179	A	27981	1	1974	
27812	58180	A	27982	344	508	
27813	58181	A	27983	3	492	
27814	58182	A	27984	65	261	

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27815	58183	A	27985	3	529	DAWAFHKMAPKAKNEAPAPP KA/EAKAKGF*RAKKGFSF*KVS HSHKKKKIPHVHPTFRAGRPL R/LRRQPMKYPSGRALPWRNKL DHLCLSIKFP/LTH*VLPMKKIE DNNTLVFIVDVKANKHQIKQA VKKL/YDIDVAKVNT/LWIRPD GEKNGICSDLAPDYDA/LDVA NKIGII
27816	58184	A	27986	105	241	PFFFFEMESPSVAQAVFSLVFRS PHCGGIQAHLFNL*RD/LFKIWT
27817	58185	C	27987	175	363	
27818	58186	A	27988	724	958	
27819	58187	A	27989	3	823	
27820	58188	A	27990	1	877	
27821	58189	A	27991	487	786	
27822	58190	A	27992	147	623	RSVAVANGLTKRRMGLKLNTRY ISLILAVQIAYLVQAVRAAGKC DA/VFKGFSGLFCSSLGDTMAQ LPAGPGDDKTNIKTVCTYWG ISHSCTV/TALIDCQEGAKNMW DKLRKESKLNLIQGSFLFCGN GNGAAGSLKLPFPVLLVSLAA LTTWLSF
27823	58191	A	27993	213	579	ASLLLLAFLAELASLKAGLQKS REYSCSSFISLSSTDAHCVLSE YARPLS/QRPAPNGSSPRCQASE AQSPGHRPPPPFSSPLAALQLD SHRFPSPDPNGKDESRPRLCTKL GRGCAGCGK
27824	58192	A	27994	1	800	
27825	58193	B	27995	54	165	
27826	58194	A	27996	46	313	
27827	58195	C	27997	30	151	
27828	58196	A	27998	169	1173	
27829	58197	A	27999	456	651	
27830	58198	A	28000	487	833	RNKFCDQDTEGNKIKNRREEK HRCRGQSKLNIIDNVVKA VNGKKSQREAEFADCIITGIRHNTS PKMSRVVRGGG/TPWAVL GMAEASSLQSSSQNPQGAGWQTGP WVVS/LGC
27831	58199	B	28001	1	2268	
27832	58200	A	28002	1	639	

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27833	58201	A	28003	1913	2388	PIIHNTTAMKKAAKAEPPTTIV CTE*AILSQRTCSL*FTVINDICP GPAH/VVQDIHGKLTGSAIA NRFQDAMAIPFLGTQGKRVRPR NGMAIPFGNRRNVIAGAFIPHR QHLGQIQLNPVRQCSNLFALHL AQRSEAFHMRRIHHRDRTVKK TILF
27834	58202	A	28004	1	1566	
27835	58203	A	28005	951	1217	
27836	58204	A	28006	1294	3108	
27837	58205	A	28007	1	1896	LFDWLVSQNELKANPAKGVSA PKAPRHLPKNIDVDDMNRLDI DINDPLAVRDRAMLEVMYGAG LRLSELVGLDIKHLDESSEVW VMGKSGKERRLPGRNAVAVI EHWLDRDLFGSEDDALFLSKL GKRJSARNVQKRFAEWGIKQG LNNHVHPHKLHHSFATHMLES SGDLRARGAYLCAKLLSGAAQ VPEWRSFAFAWFAECQEQARQN QYLQVSSC/PALEGCDVNGAS FTLEQMLAWRDHPQVTGLAEM MDYPGVISQNALDKLDAFR HLTLDGHCPLGGKELNAYITA GIENCHESYQLEEGRRKLQGM SLMIREGSAARNLNALAPLINEF NSPQCMCTDDRNWPWEIGHEG HIDALIRRLIEQHNVPVHVAYR VASWSTARHFGLNHLGGLAPG KQADIVLLSDARKVTVQVQLV KGEPIDAQTLPAEEIGRLAQFA PAYGNTIGRQPLSASDFALQFTP GKRYRVIDVIHNELITHSHSSVY SENGFDRDDVSFIAVLERYGQR LAPACGLLGSGLNEGALAAT VSHDSHNVVIGRSAEEMALAV NQVIQDGGGLCVVRNGQVTSE GAKERMGMKRYKETSGSIGLK VPAPLNLNLSLQPREQLGQST
27838	58206	A	28008	1	3257	
27839	58207	A	28009	1	2145	
27840	58208	C	28010	193	363	
27841	58209	A	28011	1	397	
27842	58210	A	28012	2	405	FVSAQPGGKRGFTAPATPGCL VHDL*APCLRWWYQHPTEELR ILAGKQQKGKTKKDRKYNGHI ESKPLTIPKDIDLHLETKSYTEV DTLALHYFPEYQWLVDFTVAA TVVYLVTEVYYNFMKPTQEMN ISLV

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27843	58211	A	28013	3	353	GYIEKRISCIALLE/SF*IPVNFLR FHDTFI*FCYSS*SIQLSLWQSQI LLCV*LLRSIDFLYLW*PLTYN EHASILSLRAPYQLFDL*NDRS HIRYSATLVNNPAVCFVAVGHD
27844	58212	A	28014	106	1814	
27845	58213	A	28015	37	2847	
27846	58214	A	28016	1	2430	
27847	58215	A	28017	1	2660	
27848	58216	C	28018	80	328	
27849	58217	B	28019	1	1074	
27850	58218	A	28020	602	853	
27851	58219	A	28021	505	649	
27852	58220	A	28022	672	1903	
27853	58221	A	28023	3	319	
27854	58222	A	28024	1	219	
27855	58223	A	28025	2	508	
27856	58224	A	28026	1	1011	
27857	58225	A	28027	1	699	
27858	58226	A	28028	175	351	
27859	58227	A	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	C	28031	115	231	
27862	58230	A	28032	2	139	
27863	58231	A	28033	1	788	
27864	58232	A	28034	115	358	LIVVRSRRGTSRSGSPRATAMA FKDTGKTPVEPEVAIHRIRITLT SRNVKSLEKVCADLIRGAKEKN LKVKGPVRMP TKVK*IVVRSRR GTSRSGSPRATAMAFKDTGKTP VEPEVAIHRIRITLSRNVKSLE KVCADLIRGAKEKNLKVKGPV RMPTKVK
27865	58233	C	28035	179	283	
27866	58234	A	28036	57	431	
27867	58235	A	28037	54	440	RVPELVWGTEVKERKNARSGV PSTQRLECGSAESAAGAPASVS VQVTAVPAFLPFGWTGGGRAV NLTEAERM RVVINSVCHWRLY E*TANRFS*KQDVGKLTNCVCH PEGMLKAVTTQAQVFLVRHN
27868	58236	A	28038	1	2693	
27869	58237	B	28039	131	350	

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27870	58238	A	28040	1	594	MLDITNDQGNASQNIINAIPPYS CKNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTP LHPPALLAVDRGSRSSVPATDS LPSAHDRQQQFHTWVCSRLLA TVRADPADGQQPARADVCGCR RGTGFNLVMIHLMGFVEGRIQ QLEQVAPRPQGVSWVEVDSSDH LQGSPRVEPPGTWDLRVLCSSQG Q*EAVNCGPQTPLD/SFDYGH SCRKVVSHCGFDLHFPDH**C KNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTPL HPPALLAVDRGSRSSVPATDSL PSAHDRQQQFHTWVCSRLLAT VRADPADGQQPARADVCGCR GTGFNLVMIHLMGFVEGRIQQ LEQVAPRPQGVSWVEVDSSDHL QGSPRVEPPGTWDLRVLCSSQG
27871	58239	A	28041	1	285	
27872	58240	A	28042	1	1059	HNLSSNSFPKMSFPNNSPAANT FLVDLSISACRSDSFYSSASMY MPPPSADMGTYGMQTCGLLPS LAKREVNHNQMGMNHPYIPQ VDSWTDPNRSRIEQPVTTQVP TCSFTTNKEESNCCMYSDKRN KLISAEVPSYQRLVPESCPVENP EVPVPRYFRLSQTATGKTQEQY NNSPEGSSTVMLQLNPRGAAP QLSAAQLQMEKKMNEPVSQGE PTKVSQVESPEAKGGLPEERSC LAEVSVSSPEVQEKESKEIKSD TPTSNWLAKSGRKKRCPTYK HQTLELEKEFLFNMYLTRER/R ALEISKSVNLTD/RQVKIWFQN RRMKLKKMSRENRIELTANL
27873	58241	A	28043	358	2292	
27874	58242	A	28044	2	300	HSL/SFFFFFFFFFFFFFFFFFFFF FFFLFFFFFFFFLLLLVFSFSFSFS SFSFSFSFSFSFSFSFFLLPSSSS SSSFFFFFFFFLLLLPFFFFFFMEH
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	
27878	58246	A	28048	3	212	

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27879	58247	A	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP NNNNNFFFFFFFFFFFFFFFFF FLLLPLLLPLLLLPLLLPLLLP SSSFFLLLSSSHSPSPSPSPSPS SPSPSPSPSSSSSSSSSSSSSS SSSSSSSSSSSFSFSFSFSFSFSF SFFFFFFFFFLFED
27880	58248	A	28050	544	729	
27881	58249	A	28051	1667	1896	
27882	58250	A	28052	1	477	
27883	58251	A	28053	25	448	RSQFFFFFFFFFFFFFFFFFFFF/ ILLVLLVLLVLLLLLLLLLLLLL LLLL/ASSSSSPSPSPSPSSSSSS FSSSSSSSSSLGAYVLYFMVT HSSPVLCCLCNLIINI*EE*FFR FRHNCDFLAASIT.GVDWLLL
27884	58252	A	28054	47	376	
27885	58253	A	28055	1	1740	
27886	58254	A	28056	3	1464	
27887	58255	A	28057	1	394	
27888	58256	A	28058	143	429	STLQKKEARARHLVTPLDILQL FNGFPLLVDCYKLLRYSRVHSF PRFWIFFSIKDHIGFPKENTQRK MRLHPPQS*TPPRE*VPSFSSG VGKSS
27889	58257	A	28059	165	408	
27890	58258	B	28060	21	253	
27891	58259	A	28061	1	150	
27892	58260	A	28062	1081	1303	
27893	58261	A	28063	147	437	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
27894	58262	A	28064	107	2499	PIEDPEGRRRMRREFILRSIQGVI. RMAPQIQPKLLTKSSTSVSQA RL/TSKQKALLPRQCSGSAKAQ AEREKIEETCQVGMKPPVPGGY TLQGKWITTCNQVQLDTIKIN GCLKGKLIYLLGDSLTRQWIYY FPKVVKTLKFFDLHETGIFKKH LLLDAERHTQIQWKHSPYFVT FQLYSLIDHDYIPREIDRLSGDK NTAIVITFGQHFRFPIDIFIRRAI GVQKAIERLFLRSPATKASVSK LKCFWEPTRGTKYEQSVTG AFPLRPKGAATPSQLVIVNSS DAHNCDEESEVRKSTLGLKL DCKKGTAITKGTKEDEEDGAM SGVDQLCLLSSVDSSGRPQLMT DWHGVKGQFSCFCGEEKELQ QKRKLTGKGWNVFFMVLEVG KTKIKALEVLASGKG TASWFIQ DFLAVNSSHGRWGKKEEFLQ KWKVDPWLPVRWELVQTGTL THLVPEGRSDSVTCAWMP LGS KQVYKEPAGFPDMLRLRGRSV RMAVVTVHSQRLNLSLGDQHF NYPLPLKKKKKKKKDTLIYPA DWLESCQSDNLSAERDLVLV LRLALCALYGLLAPGNGNTESA ELHPGDKTEAQRPMALFKVTR PLNERPGDLASHVSRFAKSLK PAMESLECPQSRVLVGEARKGHS ELVEKIERGCESTVGEGTTRKG SKRDHLDSQCKLGQRSPWQG
27895	58263	A	28065	1	1770	
27896	58264	A	28066	85	204	SPCSTSPFRQLA**RRGPHRSPFP TVAHLIGEWRLMRNAG
27897	58265	A	28067	1280	1531	
27898	58266	A	28068	1	882	
27899	58267	B	28069	77	1188	
27900	58268	A	28070	1016	1400	
27901	58269	A	28071	1091	1770	CRGGSGCAVCAELAPGAVHTV AAERAGAQEAAAGAGPPQLGG LIAWATHLQHSAAVPLLSQRM CHTCLSPRKLVI GCRAAKSLSS SPCGKWLCAALIRQPSVKGLPS CGVPLPLSLRIQMCSS EATSSW ELNPDFGEAAATSP**ESGF/LQS VVSTALLPDNTTGTFHHDGRA DIGSQFIHRLVCCHLLVLRWLI TL.DTKADVVDIGHRLRCFDCRC VDSTICD
27902	58270	A	28072	1568	1819	

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27903	58271	A	28073	778	879	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27904	58272	A	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT LKVLIIIGKLSGGRKLSRILPLLRS SSM*PTRAPN*SSASFTTTSVSG
27905	58273	A	28075	355	614	CMRRPSCSCPASTRDNTAPHSR TLKVLIIIGKRSSGRKLSRILPLLRS SSSM*PTRAPN*SSASFTTTSVSP L*NFIRLHPVY
27906	58274	A	28076	1	2226	
27907	58275	A	28077	31	117	
27908	58276	A	28078	1	547	
27909	58277	A	28079	290	730	
27910	58278	A	28080	3	267	TLVKVKDAEDQLGARVGYIEL DLNSGKILESFRPEERFPMSTF KVLICGAVLSRIDAGQEQLGRR ITILRMTWLSHQSQSKILRMA
27911	58279	A	28081	1	1785	
27912	58280	A	28082	551	685	
27913	58281	A	28083	2	211	
27914	58282	A	28084	1407	1874	PRAAAAPTNLSPELSASPRPV ACASAWGAGTDVTGWAEAMP RVGRCLPRTGLGSARRLRPEL GGGAGPAPEAMRGFGADAGST EQPRLPARS*PRLPQRRPRKRS ERPAGLAPRLRPPQPAEPPGLGS QERGRGTDRAAADPGLPTSPE SS
27915	58283	A	28085	1284	1786	
27916	58284	A	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR CL
27917	58285	A	28087	423	676	
27918	58286	A	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27919	58287	B	28089	743	852	
27920	58288	A	28090	1	1100	
27921	58289	A	28091	548	652	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY

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27922	58290	A	28092	1	2438	MRLFGYARVSTSQSLDIQVRA LKDAGVKANRIFTDKASGSSSD RKGLDLRMKVEEGDVLVKK LDRLGRDTADMIQLIKEFDAQG VSIRFIDDGISTDGEMGKMVVTI LSA VAQAERQRILER INEGRQE AMAKGVVFAENDKKMLSNFI ETADFRTLIETDRTIVVGRRGRT GSFNLAARAATRLWRYAMLME IASYISSHYKLSSQISSETLLNEH LKKWNSAQGDILRKRLVAKE YLDENNPEESIGDLQFNINISEI ENNVISLLERSDRKVILMDKL DEAYEPDNIGIGIAGLAYASIE LNQKAKCIRPIIFLRDNIFRSLSK EDPDYSRNIEGQVIRLHWDWA QLLMLSAKRMKVAFKLDIEKD QRVWDRCTADDP*KGNGFKR CLQFTLYRPRDLLSLNEAFFSA FRENRETIINTLEYAAKSISMA RLEDLWKEYQKIFPSIQVITSF RSIEPELTVYTCLKKIEASFELIE ENGDPKTISEIQLLKASGILQSL YSVGFVGIRDKNNTSSYSFCHDG RTPDKGFESNEKLLHPCYWL LNLNRNALAPEEAEEINDEYDI NIISDNSAIRNKTIGQITTHLDQI PIGNEGATEFEQWCLDALRIVF ASHLTDIKSHPNGNNAVQRDII GTNGGKSDFWKRVLEDYKTRQ VVFDAKNFEELGPSEYRQLQSY LTGPYKGLGFIINRDESEVVRSK
27923	58291	A	28093	673	916	
27924	58292	B	28094	1	4725	
27925	58293	A	28095	959	1387	CMRRPSCSPASIRDNTAPHSR LKVLIIIGKRSSGRKLSRLPLLR SSM*PTRAPN*SSASFTFTSVCS RCMSAVMVMAVLTACRFLKM TVSVGHICSLNFALQTSTTAMA VPAAATRASRAQPNGRHPWRI CWKTQKA
27926	58294	C	28096	997	1302	
27927	58295	A	28097	659	2534	
27928	58296	A	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	
27932	58300	A	28102	40	198	QAARTTGFIYHLLRHYKTPVG HS*Y*WKLHGENKSSAFVC*P TCRNPFDICW
27933	58301	A	28103	390	1186	

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27934	58302	A	28104	2	1287	GRVGFASDAQSPRILRSEPVRTP PIPAFSPKLTLRIMSLHQFLLEPI TCHAWNRRDTRPVCLDYYSLV VSFEIKK*IALSPNNHEVHIYKK NGSQWVKAHELKEHNGHITGI DWAPKSDRIVTCGADRNAVYVW SQKDGWVKPTLVILRINRAATF VKWSPLENKFAVGSGARLISVC YFSENDWWYSKHKKPIRSTV LSLDWHPNNVLLAAGSCDFKC RVFSAYIKEVDEKKAATPWGSK MPFGQLMSEFGISGTGGVWVH GVSFASAGSRLGWGSAATDSTV SVCWMPKSLQVSTLKTFLPL LSVSFVSENSVVAAGHDCCPM LFNYYDRGCLTFVSKLDIPKQSI QRNMSAMERFRNMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRKCTTGIDGAMTIWD FKTLESSIQGLRIM
27935	58303	C	28105	198	362	
27936	58304	A	28106	1	915	
27937	58305	A	28107	403	519	
27938	58306	A	28108	88	237	
27939	58307	A	28109	527	1205	
27940	58308	A	28110	2	272	
27941	58309	A	28111	39	543	
27942	58310	A	28112	1	789	
27943	58311	A	28113	401	912	
27944	58312	B	28114	147	653	
27945	58313	A	28115	586	650	KIQCLCLWLLFIIFLHAFQETIL ALRVLNVFNKRINSLGKNLAFN LFVYNKANSMP*RLWLKAPRS DK*IQ*SLRIQNQCQISSTAVH STVTKLRKSRTOPLLQQL
27946	58314	A	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL KSGSGKVYQGPAGKAADTTIIL SDEFHGRWSGASLTLLRRHSLV AG
27948	58316	C	28118	183	254	
27949	58317	A	28119	98	445	LGSGLPWENPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ACYMCRKSGHWAECECPQGIPP KPRPICVGP*KSDCSTHLAATP RAPGTPAQGSLTDSFPDGLGLA AED
27950	58318	A	28120	32	143	

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27951	58319	A	28121	39	346	QYISELQLFASTVVRQTPATSPA KNFQTPEPQQGIPPEPPPGAC YKCWKSQGHQAECCLQGPGRK/ HASHLWQPLPEPPGTLAQGSLT DSFPDLLGLAAED
27952	58320	A	28122	159	306	LGSNGLP*EINPLSSCSLFREEDP PTTSGPQTNQKEHLTNFKSAA ED
27953	58321	C	28123	80	106	
27954	58322	A	28124	166	423	RPRSERLLWGTSPSL/CALTL*G DPPITSGPQTNQLKEHLTNFKS GPHWKMDCPHTPAATPRAPGT LAQGSLLTDSFPDLLGSAED
27955	58323	A	28125	1	354	
27956	58324	A	28126	1	702	
27957	58325	A	28127	317	427	
27958	58326	A	28128	467	640	SARKRFQLSP**NKITLLKPASS AISALAAATPRAPGTLAQGSLLT SFPDFLSLAAED
27959	58327	B	28129	1	320	
27960	58328	A	28130	1	605	
27961	58329	A	28131	273	529	LGSGLPWGINPLSSCSLLREK DPLTISGPQTHQPKHLTNFKSG PH*KSDCSTAPGATPRAPGTLA QGALTDSFPDLLSLAAED
27962	58330	A	28132	459	601	DVDRHVRGNSFHHNEIRSLAAT PRAPGTLAQ/GLTDSFPDLLGLA AED
27963	58331	A	28133	112	331	LGLGLPWGINPLSSCSLLHEK DPPITSGPQTDQPKRLTNFKS ATPRAPGTLAQGSLLTDSFPDLL GLAAED
27964	58332	A	28134	1	579	
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	A	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	B	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	A	28146	1	573	

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27977	58345	A	28147	163	593	GFLEVQTPHPNLDGPRRANRN TFLWTCVGVGIDLPALPAPASFL GTQLTLKKASDGPRTKEKVTQD LAQPFWTTGRQLRFVLHLSLQQ KDLSKCWRGAEVVLGPTRLFL* GYSEGKENGTTGGVVK*AFSM CDSKWFNPCLTF
27978	58346	A	28148	159	405	PRLRVKYTQLCIL*/S/CWRERKK FHLGKRVELRQGITLGRVGVW KRRLSQGSAGCFPAGLAHSPPH LAEPAGSGFCTALFLWL
27979	58347	B	28149	123	1561	
27980	58348	A	28150	1	1771	
27981	58349	A	28151	68	698	
27982	58350	A	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	A	28154	1	245	
27985	58353	A	28155	5	422	
27986	58354	A	28156	3	1372	
27987	58355	A	28157	1	1653	
27988	58356	A	28158	586	867	
27989	58357	A	28159	1	1410	
27990	58358	A	28160	1	1441	MDIKKGITDISASLRVESGWEA RTRKEKTHINTVIGHVDSGKST TTGHLIYKCGGVDKRTIEKFEK EAAEMGKCSFKYAWVLDKLL AEREHGITIDISLWKFETSKYY VTIIGAPGHRDFIKNMITG/TSQ A/DCAVLIVAAGVGFEFESWYSP RNGQTREHALLAYTLCG*MKL IVGVNKMDSLEPPYSQKRYE EIVKEGSTYIKKIGYNPSTVAF VPMISGWNG*QHCLEAKWLTCP WFQGDGKVTP*GLAIASWEPRL LWRALALQSPPTPTDQAPLR PASPRMSYQKLGGINVATEV KSVEMIHEALSEVLPGDN/VGA FNVKNVSVDVRRGNVAGDSK NDPPMEAAGFTAQVILNHPGQ ISAGYAPVLDCHTAHACKFAE LKEKIDRRSGKKLEDGPKFLKS GDAIIVDMVPGKPMCVESFSD YPPLGRFAVRDMRQTVAVGVI KAVDKKAAAGAKVTK/SAQK
27991	58359	A	28161	125	370	
27992	58360	A	28162	156	547	
27993	58361	A	28163	108	919	

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27994	58362	A	28164	1	712	LNSEGNSSGSDSISYDAPAGNS FLEDCELSRQIGAQLKLLPMND QIRELQTIIRDKTASRGDFMFA DRLITLVVEEGLNQLPYKECMV TTPTYGKYEGVKFEKGNCVSI MRSGEAMEQGLRDCCRSIRIGK ILIQSGGETHRAQVYYAQFPDI YRRKVLLMYPILQTG\NTEFEA VKVL*DHGVHPSVILQLSPFLIP HGGQ\SHQRFPFPI*PTEVHPV APTHFGQKYFGTD
27995	58363	A	28165	1	606	GIRSAMQNTQNLQMPYGCGE QNMVLFAPNIYGLDELNETQQ LTPEIKSKAIGYLTNGYQRLN YKHYDGSYSTFGERYGRNOGN TWLTAFLVKTFAQARAYIFIDE AHITQALIWLSQLKNDNGCFRS SGSLNNAIKVNHSASFDLSI MISARMRIGSDNVKNSKGKPKQ RKIKPGWHQKRGDRTKVDCDT LSYRDGYG
27996	58364	A	28166	1	4626	
27997	58365	A	28167	15	4479	
27998	58366	A	28168	256	852	
27999	58367	A	28169	319	405	
28000	58368	A	28170	606	896	
28001	58369	A	28171	1	372	FRRVACVGSAGDITAGAEPR/G ACATAWVCEMAADISESSGAD CKGDPNRSKLDADYPLRVLY CGEYCEYMPDVAKCRQWLEK NFPNEFAKLTVENSPPQKEAGISE GGQTAGEEEEEKKQKRGT
28002	58370	A	28172	1	731	LSRGSAAAGGRALGRPWGARRV ACVGSAGDITAGAEPRGACAT AWVCEMAADISESSGADCKGD PNRSKLDADYPLRVLYCGVC SLPTEYCEYMPDVAKCRQWLE KNFPNEFAKLTVENSPPQKEAGI SEQGQTAGEEEEEKKQKRGR GQIKQKKKTVPQKVIAKIPRA KKKYVTRVCGLATFEIDLKEAQ RFFAQKFCSGASVTGEDEIIHQ DFTDAIINDVIQEKWPEVG**QPL EDLGRK
28003	58371	A	28173	335	2297	
28004	58372	A	28174	23	416	
28005	58373	A	28175	1	681	
28006	58374	A	28176	1	1668	
28007	58375	A	28177	1	1587	

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28008	58376	A	28178	250	687	AATSLPFRSTIASANSILRVGV MTSIHHFVFSKRVCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQTQIKSVRPDYLLVE PPHHMGPSPFASSGLHYDQ*PH HRLHLYWVFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	C	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	C	28181	151	351	
28012	58380	A	28182	2	355	
28013	58381	A	28183	19	428	
28014	58382	B	28184	61	2118	
28015	58383	A	28185	1	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEFG KRPAEDMEEQAFKRSRNTDE MVELRLILQSKNAGAVIGKGG KNIKALRTDYNASVSPDSSGP ERILSISADIEITGEILKKIIPTEE GLQLPSPATSQLPLESDAVECL NYQHYKGSDFDCLELLIHLQSL AGGIIIGVKGAKIKELRENTQTTI KLFECECPHSTDRVVIGGKPD RFVIECIKILDLISESPIKGR/AQP YDPNFYGWKPM DYG/GFTMMF DDRRGRPVGFPMRGRGGFDRM PPGRGRPMPPSRRDYDDMSPR RGPPPPPPRGRGSGSRANLPL PPPPPPRGGDL MAYDRRGRPGD RYDGMVGFSADETWD SAIDTW SPSEWQMA YEPQGGSGYDY SY AGGRGSYGD LGGPITTTQTIPK DLAGSIIGKGGRIKQIRHESGA SIKIDEPLEGSEDRIITTTGTQDQI QNAQYLLQNSVKQYSGKFF

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28017	58385	A	28187	221	1634	KNMETEQPEETFPNTEINGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSVDPSSGP ERILSISADIETIGEILKKIIPTEE GLQLPSPATSQLPLESDAVECL NYQHVKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECPPHSTDRVVLIGGKPD RVVECIKILDLISESPIKGRAQP YDPNFYDETYDYGFTMMFDD RRGRPVGFPMRGRGGFDRMP GRGGRPMPPSRDYDDMSPRR GPPPPPPRGGGRGGSRAARNLPL PPPPPPRGGDLMA YDRGRPGD RYDGMVGFSADETWD SAIDTW SPSEWQMA YEPQGG/SGYDYS Y/AQGGRGSGYDGLGGPIITTQVT IPKDLAG/SLFIGKGGQR/IKQIR HESGS/SSIKIDEPL/EGSEDRIIT TGTQDQIQNAQYLLQNSVKQ
28018	58386	A	28188	218	497	
28019	58387	C	28189	183	254	
28020	58388	A	28190	1	1056	
28021	58389	A	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYA EIG NR*GRNLGLTEVTGAVCEALR QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	
28024	58392	A	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN FSSFPFLVENGDAFYLAATLRA PGTVAQGS LTPSQIFSA*WRHPS ISFPS
28025	58393	A	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ SPWNSGPRLS D*LLPKSSGLSG
28026	58394	A	28196	372	782	LRSA DLPWEINPLSSCSLLHEKD PPTSSGPQTDPQKEHLTNFKSE KKETR FIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTITQHLPWSFTLSKSHFSGG RGKSLQLVPEIWPPGQMPAA QDSS
28027	58395	A	28197	189	380	SLCIFSSASALQQQWQHEGWC GQLLPRGHGPNRKLQQQRQWI LL*VPEILPGQGM PAAQDSS
28028	58396	A	28198	33	302	FRICALSTKLFCLSTPWCQTHIL SYPQYLLPLPIYVSLDLRHAFFT IALHPSSQPLFAF*TDPDTH*A QQITWAALPQGGFTDSPHYVQ

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28029	58397	A	28199	1	532	MRVRNREEGNVGVK\WGERQVD QRDAVMRVRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTTEGA GGAESISVRLPRRSGSVSLQLLS REDLGRSQSESLGPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA*QLKTD AARSPRKPDITYTFCSPGFSCTH S/SVESHNYHCSRPLQSGLPHY SRYHT*PS*LH\SLIHLTFTFPFI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRVPLVENQILTG ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFLSPCLLHCQGGKRLCG HHEEARRRKNVSI\PRKEAGIIHC KGHQK\ASDP\AQDNAYADKL AKKAASVPTSVPHGISQAPPLP THQARYWQIDFTHMPRVKLLK YLLVWVDFTGWVEAFPTGSK KATAVISLLSDIIPQFSLPTSIHS DSRLAFISQITQAVSQALGIK
28032	58400	A	28202	3	518	KRPHPYLPLTLFSDSAHLHPG EINN\HVAHTRPVWWSLHTDVH EIWCRDSDRGTS\GRSIPCPPVL CSVRKIHLQPQVLRPTS\PRNISPI LNQVSGLLSPTS\LTVPQPLS PFNLGATLQS/APFS*FQFLSFSG RDKGDTFYPWSQNSGACHRLG KAAFPWCLIIAGTPL

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28033	58401	A	28203	3	1626	SEGEAKGSITLTVCTALYLKLT LFHKTGTVFGLRFPVNTLNPS PFHDGTRELGAESAIGQCQSSA AKLRRSGKESESLGPEFQGLWK WLPSSQCFARESLLEKLSLCF RPSDPGAEPPTAVRPITERSL QGDEYCCALGGVNPWPSTDR YWNWATLQEI GPSSCRKTSSGL PLILRYGHVVDLHGSSSHHRP GPKRNKWFRELGLGSACCMRP RDLVPCVPAAPVAERGESTA QAVASEGASPKPWQLPGVGVP VGAQKSRIEVWEPLIFRRMYG KACMSRQKFAAGAGFSWYVPV AVVGAKVHDVNLHMLSFPSK WKLHTCMKFGAVTQIVTSLGR SSCSLLEKDPMLVLRPTSPRNI SPISNLTKETRFIRGPKTPAVT DWEGLPLVFNHCRDASLIHHP GFRGVRPRRDACLSPSPLANLIN LTFKVYNNRKKLQFLAFTVRQ TSAMSPAHNKQ/SLNLSGQAF LQNLPLQELATSARNPATRPRN ACSPGFLLSHVPSVRDPTGNWT VQLTWHPLPELELWPKAL
28034	58402	A	28204	921	1009	
28035	58403	A	28205	1	1005	
28036	58404	A	28206	1	2706	
28037	58405	A	28207	1336	1490	
28038	58406	A	28208	466	560	
28039	58407	A	28209	863	1672	
28040	58408	A	28210	1	876	
28041	58409	A	28211	133	746	SVKMVRYSLDPENPMKSK/S QRGSNLRVFPKDH5*KLQPAHQ RVCHIRKSPTKY/LKDVHLTRN QCVPIPDYNG*QLGGVCRRPK QMGPGTTKGR/WPQKGVLFKL PAHALKTAEM*C*TLRVLDVDS LVIEHIQVNAKPKMRRRTYR AHGRINPYMSSPCHIEMLTEK EQIVPKPEEEVAQKKKIS/QKKL KETPLTWHGE
28042	58410	A	28212	3	466	
28043	58411	A	28213	1	2772	
28044	58412	A	28214	1	1353	
28045	58413	A	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR S*DY*CWR

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28046	58414	A	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEKASSQATLPNQPVKEAI IMQLGTLTLTFLHELVPPTALPSGS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQKIWNSW*SC LVLI*PPCVILSFLYVQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
28047	58415	A	28217	2383	2651	
28048	58416	A	28218	125	1396	
28049	58417	A	28219	466	643	
28050	58418	A	28220	73	150	
28051	58419	C	28221	1	240	
28052	58420	A	28222	2	499	
28053	58421	A	28223	192	351	
28054	58422	B	28224	1	2103	
28055	58423	A	28225	247	400	
28056	58424	A	28226	288	589	WCSRRRGWYLLLGFNHYWRSS TFLVRCPTSPCGGCCPRYGIYPV RSCPRLPGGVSRYGSIHSG/RWC SWSPSWPWLTSVTPRLYVAL M*AVVCPVVGKQF
28057	58425	A	28227	319	398	
28058	58426	A	28228	1299	1506	
28059	58427	A	28229	1250	1907	
28060	58428	A	28230	547	638	EKRKSNCPCLQMT*LYI*KTPSS QPKISLS

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28061	58429	A	28231	488	2358	RLSLGHWAAAGKQGASDSCKEP TQPPSGVLESTTP/CAAPSPPNR DSGPCPASSPLSRLLSGTAW APPPAPPWARVRPPREVRAD LLTPQGGGPATGVSGGECDSP VGGNPGIWKAWGHRRTVRAGI GRRGGPGGADKQPLLVLRLQTG SGVDLQQTPTDLQLRVLTVRR NTNKRKGHPHQNPICSTPSSKT EGRSMRQKVNKDIQELNSALH QVDLIDYRTLHPKSTEYTFSSA PHHTYSNIDHIVGSKALLNKCK RTEIVANCLSDHSAIKPELRIKK LTQNCSTTWKLNLLNDYWR SKRKTHSKASRRQEITKIRAEK ELETQNTLQKINESRSWFFENIN KIDRLRLERLIKEREKNQIDA NDKGDITTDPTKIQTITREYYKH LYKNKLLNLEEMDKFLDTYTL PRLNQEEIESLNRPIGTYEIAII NSLPTTKSPGSDGFTAIFYQRY KQELVTLFLKLQSTEEKILPN SFHEASIIILPKGRDRTTKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHDQLGFIPGMQGLFSTC KSNVIHHINKTKDKNHMIIISID AEMASDKIQPFMLKTLNKLGI DGMYLKIIIRAIYDKPTANIILNG
28062	58430	B	28232	1	2664	
28063	58431	A	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPACPKRAPE GSTKHGKEQPVPAATAKTQIV
28064	58432	A	28234	804	920	RDIYSNKCQPEKPEKI*NGHPNI TIKRIREARAKTFKS
28065	58433	A	28235	786	935	
28066	58434	B	28236	3	1555	
28067	58435	A	28237	895	1389	GELLEVMTLAWSWGLFLARII QTQVFKAFNLVILIRSSWAF WTHGDELWALVSRKPK*HPGF CDHAPSTFPPGLCP/EPTPPGA VSQYPCPPSPCWPRWLVLPLP VLAGTSSPWKGFSYPPCCFSPF HLPARFLHRGNCLSTFDLVVLP PLEMPVLALS
28068	58436	A	28238	704	799	EKRKSNCLCLQMT*LCI*KTSPS QPKISLGW
28069	58437	C	28239	178	1287	
28070	58438	B	28240	1	1028	
28071	58439	A	28241	476	678	
28072	58440	B	28242	1	1059	
28073	58441	B	28243	1	924	

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28074	58442	A	28244	39	200	LPLFLIECLFPSPA*LPWPGLPTLC*IGVVREGIPVLCPFSGMLPVFAHSV
28075	58443	A	28245	225	314	
28076	58444	A	28246	243	311	
28077	58445	A	28247	21	1593	KKRTAPAGPRRHPKHCECPNCGSGKGRPS/CSQTHPPGKLKSSP*SRKAENSKNQSAFSPPKDHSSPVMEQSWMENDFDELTEVGFRSLAETQQQKQKFRPISLMNIDVKILNKILANRIQQHIKKLIHHDQVGFISGMQGWFNICKSINVIHHINRTNDKNHMIISIDAFAKFDKIQQPFMKLTLLKLGIDGTLYLKIIIRAIYDKSTASHLNGQKLEAFP LKDRTRQGCP LSP LFNIALEVLARAI RQEKDIKICLGKEKVRLLSFAEDMIVYLENPVSAFNLFKLISNFSKVSGYKINVQKSQVFLYINNRRQESQIMNEFPFTIARRRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKMPSCSWIGRINIMKMAILAKVIYRFNAIPIKLPMTFTELEKTTLKFIWNQK
28078	58446	A	28248	129	239	FFLTMSMECSSICLCPPLFR*AVVCRSP*RGPSHPL
28079	58447	A	28249	3	254	GTAWAPPPAPPWAVRVRPEKCGAPTCSHPREEAPRLASPAKGNVTPVWGETQSGRLGVTGEPELLGLGGAGALARLISSLCW
28080	58448	A	28250	80	517	GHFLGQQPRPQLHSPAPDPPAPTPTDAEGLPQQQLPQLEPQPECQGPVVEAEARQLKSCMKPVRRRPAEEELKTKNMDDNTFAMAEHPDVQESVGLVAITPLRPWPQMTLQVCWSLLEFHSRPLPGYHQQLQNSKDCCLFLP
28081	58449	A	28251	1	670	
28082	58450	A	28252	1450	1650	QWISRQKLYKPEESGGQYSTFLKKRIFNPEFHIQPN*AS*VKEK*NPLQTSKC*EILSPGPLPYKSS
28083	58451	A	28253	1010	1294	QRFWSQKLYKPEESGGQYSTFLKKRIFNPEFHIQPN*AS*VKEK*NPLQTSKC*EILSPGPLPYKSPESAKHGKEQPIPTAKTCQIVKTIQA
28084	58452	A	28254	41	812	
28085	58453	B	28255	1	2957	
28086	58454	B	28256	650	3212	
28087	58455	A	28257	1	556	

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28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA SRDSS*AVSHLCGTPLEIGWSNL PGSHSQSPWNSGPRLS
28089	58457	A	28259	1	253	
28090	58458	A	28260	409	884	
28091	58459	A	28261	1	2256	
28092	58460	A	28262	118	302	
28093	58461	A	28263	558	659	
28094	58462	A	28264	1	400	
28095	58463	A	28265	308	433	
28096	58464	A	28266	1	711	
28097	58465	A	28267	559	657	
28098	58466	A	28268	1	400	
28099	58467	B	28269	232	498	
28100	58468	A	28270	1	2978	
28101	58469	B	28271	128	290	
28102	58470	A	28272	3	193	DVNIFIRYGLWCFLSPFGL*QF WRLEVQYQDAADSMSSGGDPLS HS
28103	58471	B	28273	125	197	
28104	58472	A	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGKNNGGEASM VRGCLERAET*GCPNGMPQGE RLSRFGLRTETGTVTFLHCL QQSR
28106	58474	A	28276	3	334	
28107	58475	A	28277	2	1698	
28108	58476	B	28278	1	1281	
28109	58477	A	28279	198	532	NSLFLLLCLQALVSG*CWPHK MS*GGFPLFLLTGIVS/GRNGTS SSLYLW*NSA/VNPSGGPGLFLVS RLLTIASISEPVIGLFRDSTSSWF SLGRVYVSRNLSISSRFSLLFA
28110	58478	A	28280	3	610	TDFCFFWLPGLSVLFLSFFLSF FLSFFLSFFLSLFSFSLFLFLS VLSFLPSFLFLSLSLFLSLFS LL/YCLSLFLSFFLFLSFLSLS SLLFSLLFSSLLFSSLLFLLLLL LSLSLLFSLFSLFSESVLWEGSV AGLQTPALSSALNRAVLPVSCS MIDQLCDPGKYFISLCLFLHLR VRTCGVWFSVLVIVC
28111	58479	A	28281	203	470	QAKSVVWKILSFRI*LHRMSDG IFWLCFYISMHLCLWLVLYWAV WFKLQTTIRSLRWLTDSPVSVY GYCQGMNEGCSQFKTVPTLFS SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK EISKGLTKTPRLVMSPPSSCSR RGIWPNPDTCLLLLL
28113	58481	C	28283	1	603	

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28114	58482	A	28284	179	445	QLSGLASGMRESRDVGLRFTPLLLWIVHSRAWLVESAVMSTWECWVGDERGTGVKLAGAHTELPTGPGV*YSPPCVHVFLSFLNSHL
28115	58483	A	28285	128	381	
28116	58484	A	28286	1	1392	
28117	58485	C	28287	1	3169	
28118	58486	A	28288	1905	2449	AQLPTAPLPFLGRRWGTWGFPGHAFHSWFWYSTGEGAMGSFLALLSFPLGMKLAILEDFFGISGTAAPLGGSSFGSSLRSSLSVTEALLARSL/HFLILLPLFLLLFLIAFQRTLLVGQCPAKSPLGNALECNLGAAGSRAHGGEHATGGLQLLALFEAGQSLQPLTACVPGPRPLTCL
28119	58487	A	28289	693	905	EESIS*KWPYCPSFHNHPQAYKAIPHPASLGK*YQNQDNNNAGKLFKANRNPAIGCQQPVCSTKDGRF
28120	58488	A	28290	3	427	
28121	58489	A	28291	1	1195	
28122	58490	A	28292	158	779	
28123	58491	A	28293	227	378	
28124	58492	A	28294	1	621	
28125	58493	A	28295	1	351	
28126	58494	A	28296	1	507	
28127	58495	A	28297	1	543	
28128	58496	A	28298	343	428	
28129	58497	A	28299	785	1178	

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28130	58498	A	28300	842	2592	IREEVESLKRPTSSDIEAVINSL SIKKKVQYQTDSPQNSTRGENL GNTIQDTGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TIIRVNRQPTWEKIFEIYPSNK GLISRIYKELKQIYKKKTNDPIK KWAKDMNRHFSKEDIYAAKK H/DEKMLIITGTWMKLETILSK LTQEQTCKHRMFSLLIPDDGNS LTRRMLLIGISVKTPVGTGAIPG PVGGTAAAGAYGRKEKALSNC DSILALALAKMSENQMSMESFF EKGKDPMRQKQKTLTLTKKKN AFKRKYQESYLNFGIATVRAS FLVANCIVKAKKPFITGEELILP AAKDICYELLGEAAVQKVPHV PLPVSTITRPIDEIAEDIAQFLE RINESLWYTIQIDKSTIADNKAT MLVFVQYIFQEDVHEDVFFQES LRATSQPLKTPQTGKEWVHDPF VDKPSSESTLSMLEEDQLEIAN DGLSKSMFEKTSNLHIVCIKVK AEYPEIATKALRRLLAFPVWAA VDRECQWGSRDVEMRRLDPK AGFSLGVGNCCHCLRTLEFVGL SMSSLCGAMLLCGLRAAPYISL RDHKGQGTLL
28131	58499	A	28301	1	1662	
28132	58500	A	28302	2	406	CWWDCKLVQPLWKSVMRFLR DLELEIPFDPAILLGIYPKDYKS CCYKDICT/RVCPVAALFTIANT WNQPKCTSMIDWVKKMWHIY TMEYYAAIKKDEFMSFAGT*M KLETILSKLTQEQTCKHRMFSL YWKs
28133	58501	A	28303	1	1404	
28134	58502	A	28304	68	2269	

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28135	58503	A	28305	189	1890	MKMASSLAFLLLNFHVSLLLV QLLTPCSAQFSVLGSPGPILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDRQSAPYRGRTSILRDGITAG KAALRIHNVTASDSGKYLCYFQ DGDIFYEKALVELKVAALGSNL HVEVKGVEDGGIHL ECRSTGW YPQPQIQWSNAKGENIPAVEAP VVADGVGLYEVAA SVIMRGG GEGVSCIIRNSLLGLEKTASISIA DPFFRSAPWIAALAGTLPILL LLAGASYFLWRQQEITALSSEI ESEQEMKEMGYAATEREISLRE RKKIQYLTDPVILYPDMANAIL LVSEDQRSVQRAEPPHDLDPNP ERFEWRYCVLGCEFSMERHY WEVEVGDRKEWHIGVCSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTEPRTNLKLPEPPR KVGVILDYETGHISFYNDGDS HIYTFHASSSEPLYPVFRILTLE PTALTVCPIPK/GREFRPFPTLVP DHSLEIPLTPGLANESGEPQAEV TSLLPAQPGAKGLTLHNSQSE PYSYRHTLKHFTDIHSIIP

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28136	58504	A	28306	172	1905	MKMASSLAFLLLNFHVSFLVQ LLTPCSAQFSVLGPSGPILAMV GEDADLPCHLFPTMSAETMELR WVSSSLRQVVNVYADGKEVED RQSAPYRGRTSILRDGITAGKA ALRHHNVTASDSGKYLCTYFDQG DFYEKALVELKVAALGSDLHIE VKGYEDGGIHLCECRSTGWYPQ PQIKWSDTKGENIPAVEAPVVA DGVGLYAVAASVIMRGSSGGG VSCIIRNSLLGLEKTASISADPF FRSAQPWIAALAGTLPISLLLLA GASYFLWRQQEKIALSRETER EREMKEMGYAATEQEISLREKL QEELKWRKIQYMARGEKSLAY HEWKMALFKPADVILDPDTAN AILLVSEDQRSVQRAEERDLP DNPERFEWRYCVLGCENFTSGR HYWEVEVGDRKEWHIGVCSK NVERKKGWVKMTPENGYWTM GLTDGKNRYALTEPRTNLKLPE PPRKVGIFLDYETGEISFYNATD GSHIYTFPHASFSELYPVFRILT LEPTALTICPIKEVRRVPPI/AD LVPDHSLLEPLDPA*LMKVGE PQAGK*HLCFSLPTLGAELPLF
28137	58505	A	28307	1	2220	
28138	58506	A	28308	134	509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAQRSP AEKMGETPGAASVSRILGGRV ALRRHVGRGELRAPDCLGPD WVPTRGSHFGFFPREQSL/W GATPPSYRSSEVRSGAESGRAP DSVSGSVQAH
28140	58508	A	28310	1	1066	
28141	58509	A	28311	77	273	
28142	58510	A	28312	1	415	
28143	58511	A	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	A	28315	2	671	PGEFTRAPRVRRRAMGISRDN WHKRRKTGGIRKPYHKRRKYE LGRPAANTKIGPRIHITVVRG GNKKYRALRLDVGNFWSGSQ CCTRKTRIIDVVYNASNNELVR TKTLVKNCIVLIDSTPYRQWYE SHYALPLGRKKGAKLTPEEEI LNKKRSKKIQKKYDERKKNAK ISSLLEEQQQKLLACIASRPG QCGRADGYVLEKLEFLYLRKI
28146	58514	A	28316	3	1259	
28147	58515	A	28317	1745	2681	

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28148	58516	A	28318	1	2502	
28149	58517	A	28319	1097	1417	
28150	58518	A	28320	1	398	MTAEERDKFPTDQQAIPSMDPH WDPSDSHDGDSHKKHLLTCVLE GLRRIRKKPMNYSMMSTITQG KEENPSAFKWLREALRKYTPL SPNSLRGQLIKDFTITQSAADI RRKLQKQALGPEQNL EALLNQ ATSVFYNRDQEEQAQKEKRLSS RSVTIRGILGQSVTRPEAHKGL QDIVKHLKAQGLVRKCSSDCN TPILGVQKLNQWRLVQDLGLI NKAIIPLYPVVNPYTLLSQISEE AEWFTVLDLKD AFFCIPLHSDS QFLFACEDPTDHTSQTITLPH GFRDSPYLFQQALAQDLGHFSS SGTLALQYVDDLPLATSEASC QQATLDLNLNLANQGYKASRS KAQCLQQRDGGQTTLYSNQGA PEGKYSSSRMRPVRNSLQNLK AGPSTTPALSLPTGQNL SLYVT ETAGIALGVLTQA HGMNPQPV AYLSKKIDVVAKGWPHCLRVV VAVAILVSEAIIQGGDLTVWT THDVNGILGAKGSLWLSDNCL LRYQALLLEGPVLQIPMCAALN PATFLPEDGEPIS**PLTLRWPLP QLPLNSEASLLHQS FSYLGMP LVGSSSHEPA
28151	58519	A	28321	318	363	
28152	58520	A	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP PLPARWPIH
28153	58521	A	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD TSEHLKEQTADTSSSLRTVTLTA RVCGFILEVSETKNSPEGTNSG HILTSQMGLSPIAKRRETSASAA ALVSATIPICRVQGPLRVLGQE VFLLLLRLPTA PLPINDKPP/PN/ TPLPRRKQAKKSPDKHKNPWAI GYVPFKQ*GEGNLA*PGYMSPS

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28154	58522	A	28324	350	1563	FLYIQLYPTPITCSLKYQRKQNG SLFWTSRMPSSVFPCTLTPSFSL PLRIP/PDHTSQLTWTVLPPGFR DSPPLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSSEASCQQA TLDLLNFLANQGYKVSRSKAQ LCLQQVKYLGILAKGTRALIK ERIQPILAYPCPKTLKQLRGFLG ITGFCQLWIPGYSEIARPLYTLIK DTQRANTHLVWESEAEAFK TLKQALVQAPGLSLPTGQNFSL YVTERAGIALGVLTQTRGTTTPQ PVAHLSKETDVVAKGWPHCLR VVAAVA VLVSEAIKIIQGGDLIV WTTHEVNGILGEKEVYGYQTN AYLDTRRSALRDWCFKYARPV AAIILLALAFGPCINLPVKFVSS RIEAIKLMVLQMDPQISSTNN FYRGLD
28155	58523	A	28325	830	1143	
28156	58524	A	28326	234	510	PWQSLP*VAQKVPKDHRSLPLE P*TRSLNNS*QHWLCPPARAP STCSTSCPARDGPPPPSPAPHGP RNTSVPGVHSRGPSPPPRTPPP VS
28157	58525	A	28327	2	816	
28158	58526	A	28328	1	1311	
28159	58527	A	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	1	484	
28162	58530	A	28332	72	299	
28163	58531	A	28333	737	847	
28164	58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	A	28339	65	244	
28170	58538	A	28340	2	584	GKSRMFPAQEEADRTVFVGN LEARVREILYELFLQFLIAGPL TKVTICKDREGKPKSFGFVCFK HPESVSYAIALNNGIRLYGRPIN VQYRFGSSRSSEPANQSFESCV KINSHNYRNEEMVVGSSFFPM QYFPINNTSLPQEYFLFQKMQR HVYNPVLQLPPYEMTAPLPNS ASVSSSLNHVPDLEAGPSS

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28171	58539	A	28341	2	367	MTMHYEIPVTRRSKGT*LPQ NA/SVNNMPH*TGAI*ADISM TN YARIERNHLGRGNSNSKDPKLR ESSEHLRKLKTRVVNEQTRLGL IMETVVGGRGGEAPFYFQCDKHL SRSPQGLGLICL
28172	58540	A	28342	98	387	RKQPPKVLQWLLAF*SHRSW LSSPWPSDLWRPWAGGACARL LLQQPRDSASLKERQQPSGAY R*NSHLPGEHLGEGVAVCAAS ADLNVTAACWL
28173	58541	A	28344	1	269	
28174	58542	A	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	A	28347	59	310	
28177	58545	A	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQ LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC DVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSFLSVSKNIFI SAFISLCTQ*SFRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQCGQFW NRCGVVLKKMYILLIWGG EFC RCLLGLLGAELSSIPGYSC
28178	58546	A	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQ LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC DVR VSISDLSCFPLWAFSAINFPLHT ALSASQRFWYVVSFLSVSKNI FISAFISLCTQ*SFRLFSFHV VER ERL*VRF/CNPEF*FDCTVV/WR *FVIVSVLLHLRRLALLPTMWSI LE*VWCGAEKNVYSVDL GWR VL*MSIRSAWCRAEFNSWV SLL TFCLVDLSFSLAALNIFSFISTLV NLTIMCLGVALL EYLCGLVCI
28179	58547	B	28350	1	3135	
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNQ LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC DVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSFLSVSKNIFI SAFISLCTQ*SFRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQCGQFW NRCGVVLKKMYILLIWGG EFC RCLLGLLGAELSSIPGYPC

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28181	58549	A	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCVDR VSILDLSCFL*AFSAINFPLHTA LNASQRFWYVVSLSLFSKNI SAFISLCTQ*SFRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFPVCGQFW NRCGVVLKKMYILLIWGGEFC RCLLGLLGAELSSIPGYPC
28182	58550	A	28353	1	3531	
28183	58551	A	28354	1	3126	
28184	58552	A	28355	2357	3083	FFSLFFFILASGLSILLIPSKNQL LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCVDR VSILDLSCFLWAFSAINFPLHT ALNASQRFWYVVSLSLFSKNI ISAFISLCTQ*SFRLFSFHVVE RF*VRF/CNPEF*FDCTVV/WRD SLL*FLFFYIC*GELYFQVCGQF WNRCGVVLKKMYILLIWGGEF CRCLLGLLGAELSSIPGYPC*FF VLLICMLTVGC
28185	58553	A	28356	6412	7092	FFSLFFFISLASGLSILLILSKNQL LDSLSF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCVDR VSILDLSCFLWAFSAINFPLHT ALNVSRFWYVVSLSLFSKNI FISAFISLCTQ*TFRLFSFHVV ERL*VRF/CNPEF*FDCTVV/WR DSLL*FVFFYIC*GELYFQLCGQ FWNRCGVVLKKMYILLIWGGE FCRCLLGLLGAELSSIPGYPC
28186	58554	A	28357	1	2019	
28187	58555	A	28358	1	1263	
28188	58556	A	28359	77	304	
28189	58557	A	28360	1	756	
28190	58558	A	28361	1	369	QQRLLASNEAFKSAKASQSP ASKYMKENDQLKKGAADVGG KLDVGNAEVKLEENRSLKAD LQKLKDELASTKQKLEAENQ VLAMRKQ/SPEGLTKEYDRLL EHAKLQAADVGDPMDDKEE
28191	58559	A	28362	879	1156	
28192	58560	A	28363	54	407	

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28193	58561	A	28364	620	1246	GSTWHGWDGSRCSRQNRWSC MTKRSSQPSSL*SRRRRWMS SSPNW*KTGPSSMSRMSSAG* SAASSRSCATRWTRRRPAAWR G*GVTPVAWWPPWTCWSRPR EPGSGWPKPSVCWNSSEMRTT MSSSGSSTPWPPVSRRRPWTER RLGSRGDRRLRERSRPAVNRT RMSRVPSGAPRGTPSRWWMM MKCWDHQMRGLVEEVG
28194	58562	A	28365	86	402	KGWCCRKGWNRKSWFLT FLQGLLEGPHPSPTAPRRTT* SLYSAPSRMVQLDDLLHKWF LYSCLVSAISIGIKFPLKIHISPG GVLEARETMSHFKEAAL
28195	58563	A	28366	54	353	
28196	58564	A	28367	66	352	
28197	58565	A	28368	442	700	HWNKVPAENPHLPWVRCSPT PLGKPKPCSSWNRSGTDVSGT GLSEGSWSWPSGSCNGVTGTDA YGP\GYVKSGSFPGRVRGTV
28198	58566	A	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR SKDATPDPPRGLGKFPPLPQA PRLGSRLLSTLCSTLSGRGG KNTSRLSFSPSGSVKGRVRDVK EPGPIRAHRTAFFPNASS/GSEG R*SPSVVAVRGRF/CVGVWRFP TVGVVWHAPRCTR*SPITGSAP LSVWSPACTGSPCTAGA
28199	58567	B	28370	163	387	
28200	58568	B	28371	112	419	
28201	58569	A	28372	1	1902	MSRIA WKLWKLIQGYLGQPA GTARRHPGIGFKSPPGDFTCNG LIAVIKQSDNQRMSPGWSW GRENNPTLVEVLGVRLPETV HTAVRYTSIELVGEMSEVVDNR PQFLDPVLGYLMKGLCEKPLAS AAAKAIHNICSVCRDHMAQHF NGLLEIARSLDSFLSPAAVGL LKGTALVLRPLDKITECLSEL CSVQVMALKKVFGATSRRA KLFRGLKAHGNSFETSGEAER CCTWRPKEMTCVE
28202	58570	A	28373	1	2019	

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28203	58571	A	28374	2	1455	SAAVAARSPPQRPSPATLGGPG QRRPPSAAPTAWAAAAAPGS RRRRPLPARPLWAPARGAAAA GPAEAPMLARRKPVRAALTINP VITAEGSPVITSEGAASEANLGIDL QKKLEELDEQ/QKKRLEAFL TQKA/RRVGELKDDDFERISEL GAGNGVGVVTKSPAQDPSPGLIM IARKLIHLLEIQAGASGNQIIPR/D LQVLHDGTWPTMGGVFGAFY SDGEISICIEHMDGGSLDQVLK EAKRIPEENLGKVSHSRFSGGL AYLREKHQIMH/RDVKPSNIV VNSRGEIKLCDFGVSGQLIDSM ANSFVG/TRYCMAPERLQGI/TH YSVQSDIWSMGLSLVELAVGR VPIPPRDAEELEAIFGRPVVDG EEGEPHSISPRPRPGRPVSGHG MDSRPAMAIFFELLDYIVNEPP KL/PNGVFTPDFQEFVNKCLIKN PLAERADLKMLTNHTFIKRSEG EEVDFAGWLCKTPAG*TKPGTP VTRTAV
28204	58572	A	28375	229	257	VSLSASPLVSLAGRSPRLGRG CQSLDGYGVGWQAQSPGADE GNRSFT*PELADKNVPNLHVM KAMQSLKSRGYVKERLPSSAP GDCACHPT
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP KQKQ*PGGTEDS/YDASGPPPKF LIKEIKLGVPFRFFPIRGV*NPGPG KNFGGPFKKT*FCWARVPKM* FFKGGPSSSSPAVSLFNAKESPI LLRWMTSTTSKAYKLEFGC
28206	58574	A	28377	1	367	
28207	58575	A	28378	1	1001	MSWEMEQDEVYKEMSINHKN EGTRVEKPNRYRIIHQPDAINH VSRKKDVPSASGAGHSRSSTGS RPGVRRLWPLLLRSAPSGPLNN AVPAPGKGPGRWGGSPSLRSRG GKASTRVAPGLSAHSQAASGV PEPAEPQHRTKASGSRRLSLR VVPEAPKPRTRTAREGKGAGA GHTGGAQEQRRRRRWACRGLR GRPGAVSPGGAEAINQLASEHC GNPAAALHRCIASLPRNLLVW AGRMLMPKKNRIAIYELLFKEE VTVVKKDPVHMPKHLEADKNS RGYYVKEQFAWRHVYWYLTN ED/MPVSP*LPSAPGDCACHPT PQPSRDWQASV

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28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG ADEGNHGDGTGYPHW*GTSRNV SRQTVQTRSLGT
28210	58578	A	28381	168	378	
28211	58579	A	28382	1	900	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILPL FADKVPKTAENFRALSTGEKG FGL*GVPCFHRUIPGFMCQGGDF TRHNGVGGKSIYGEKFEDENFI LKHTGPGNLSMAKCDPTQN GSQFFNLALAKTEWLGWASHV GVLA*KKGMNIVEAMERFGS RNGKTSKMITTADCGQLRIKFD LVFYLNHQDHSFWKPQGEHPS NPFARRILRLWLSLAVPFWVPC FPCSLPCLAGLQS
28212	58580	A	28383	393	683	HAKDGMEOGRNNECPKVGGKQ VTLQHSDEDRKTSRGENLY MSSDPTSWSIAQSWYDEILD VYGVGPKSPNIVLLVII*HIERIPR TNKEHLVVP
28213	58581	A	28384	119	193	
28214	58582	A	28385	1	567	
28215	58583	A	28386	957	1145	EQNLLIYLVSIQDCMDKGCII* LRHTSGNCMYVSDKDFDKEQCI FSRSSHQSLSGNDLQK
28216	58584	A	28387	153	2257	
28217	58585	A	28388	369	539	KKPARRRHFLTLLCCVFSPKLC TAGGPMRRTFKSYDEAGTGLL SVADFRTVLRQYSINLSEEFFH ILEYDKTLSSKISYNDFLRAFL Q*TPKL
28218	58586	A	28389	3	1364	
28219	58587	A	28390	1	996	
28220	58588	A	28391	296	549	ETSSSVTVSDPEMENKGGQTLA NNSSSLMAEAPGTMCRFTLAPH VLAQVGTITDLPDHLLSYDGSE NLSRFWYDFTLENSVLCDS
28221	58589	A	28392	1	1065	
28222	58590	A	28393	412	428	WILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPLPARWPDLSL MQLARQVSRLESGQ
28223	58591	A	28394	3	505	
28224	58592	A	28395	1	1201	
28225	58593	B	28396	518	1606	
28226	58594	A	28397	1	798	
28227	58595	A	28398	737	3067	

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28228	58596	B	28399	133	239	
28229	58597	A	28400	3	376	
28230	58598	A	28401	1	1194	
28231	58599	A	28402	405	611	
28232	58600	A	28403	204	4198	
28233	58601	A	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMTFTITQLLVVEV KDSLERLAVEVVFILQKAMY KQAHYIMKSLCPQMVLMLRFI QWVQIMPMLKLENLQHLMAR WNETVKEKK*D'LLFSMHERN
28235	58603	A	28406	359	517	
28236	58604	A	28407	68	487	
28237	58605	A	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQTEQPSWLHPVDP APGLQVELPASHAPCARTPQPL GGRWDWAPWSRGWCSLGRLG PHRSPWSGWAEQA*QWIPHQ CRWSCLPVTTRVLALLSPWV DGTGRRGAGGARWGGSGRT GAHGVGGRLRHSRLQVPSPAL LFKYYVCDFK
28239	58607	A	28410	1	609	MVFSNLKGHWLQPIRLDSGSR NTAIGCDNQYKPTGVKLQTF VSVTALKAAARLGLFVPPGGLV VSLGSGVKLQIFASQVVCDFRA LIGAFTIPELDTKVLHVPIRLVR YRVVWTRFSKAPPDSSGAQLASP SESHTRAAGGAACQSQCRAPA LLSPWVVDGTGRRGAGGGAHR GGSGCTGTHGVGGRRLRHSGLQ VPSSA*VSHPLRGFL/LQPEPR* APPPAPRRPVPSTTQGLRSAGA RHWWDQAAPPAALVWDSLGE ASWAPESGGALENLCVHTLYL TNLMGTWRTFVSSGIVNAPIS ALSKQTTWLAKICSFTPEPRETT SPPGGTNNPRAALRAVTLTAK VCSFTPVGLYWLSQLPMAVLE PESNLIGWSQWPFRLKT
28240	58608	A	28411	548	753	TLLWE*SRLRKKSHLMMTLNH STHSITFGLDKHCASYLMGFLYI VELLIAQCGSPGATLIQWRMAS MD

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28241	58609	A	28412	1	903	MAKKIQLTYKCVQNWVVLGLTDFKNEAADPRRVKLQTFVVSVTALKAAARLELFIPPGGVVSLASGVKLQTFAVSVTAHKGVSVDPKTRHKGSPSPHQIQEPSWLHPVDPAPGLQVELPASPAPCARTPQLGGQWDWVPWSRGRCSSGRLGPRSSPRWGAGSGMAGCRSRALPHGEAAAKARQKVTAAGPGAKHLTAWGWQGQLATPSVGPAEPTHTQNSHWPAASVCSPSSRLRLSLHTYPQAEGAGSGLGQPRKGLPQCSSLKGSSSAAKVGAQAEVVPRASEACEG*RAPQVLPKWEPRQRRCRERARPARAASTLSPLISI
28242	58610	A	28413	1178	1480	CRHLIQSHSICLHQWDCHTQHL YHPQ**WNQQQLHHRCLLQGSIHLVFGPQWDPRRRRPLRGTRSAMARMDILRISREYITQEITEAATKRKVLSPKE
28243	58611	A	28414	126	407	WIPHRGCRWSCLPVPCRALALLSPWVVDGTGRRGAGGGARQGWGSTGAHGVGRRLRHGGGLQVPSPAPRESS*GPARNRSQRRRS DSSLRERK
28244	58612	A	28415	27	363	
28245	58613	A	28416	1	576	
28246	58614	A	28417	813	923	YSLIHAAPQQR*SLSGPHQTYDISSYTQCCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVPTRLRSPASFTQWIPHWGCRWSCLPVPRRPALLSPWVVDGTGGCGAGGGAHRGGWGCTGAHGGGRLRHGGGLQVASPAPREGS*GPARN*AQSRWAGTAGGSPSTPSAAGPGA PLIAPGRQGNPECHWCGARQAHAPQLATASASWTRAFRECVPSPWPSCLGAACFVCLLIGPFPFFSQQHLSTSLGHLVLLSWHLTSLSVSFRILTRLRLRVFTGSWGGGAA
28248	58616	A	28419	1	616	
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28253	58621	A	28424	1300	1648	
28254	58622	A	28425	1	599	

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28255	58623	A	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK YVGLWDFKSRDDELSFRAGD VFHVARKEEQWWATLLDEA GGAVAQGYVPHNYLAERETVE SEPRDQTQAVRHYKIWRAGGR LHLNEAVSFLSLPELVNYHRAQ SLSHGLR
28256	58624	A	28427	3	438	
28257	58625	A	28428	37	403	
28258	58626	B	28429	1	1176	
28259	58627	A	28430	2	2150	
28260	58628	A	28431	1593	3025	
28261	58629	A	28432	322	2168	
28262	58630	A	28433	183	591	
28263	58631	A	28434	2	258	
28264	58632	C	28435	52	363	
28265	58633	A	28436	1	3363	
28266	58634	A	28437	1	918	
28267	58635	A	28438	1	1422	
28268	58636	A	28439	3	10899	
28269	58637	A	28440	277	586	
28270	58638	A	28441	3	3364	
28271	58639	A	28442	1	1851	
28272	58640	A	28444	3	253	CGIEDNNFSLALNPDTILLS/HS GGRGAEAPTMCCLKTVSKRAC FEGLEWQFNLWRNKK**C*DK KHKTAGCSIS*VMRSVYR
28273	58641	A	28445	1	950	MGSSAVQSQAALAPRVLTTG LADVTALLRAPATPGRVLVAGA RGGWGYVQSCRGAGAAVKP LGSAETAVPARLGCRRFSRSC CRRRGRGSLLSFSAAKPIVFKEK LTMKTDSLMEEKLECSLWCCL SDPSTPGRCVLERRJPWMQ LLANIKQAEKHEKNHPEVTVA MALTDIDLQLQFSMSQPE/GPPS PGSRPS*PPAAALLWTPAGQA CPGPGGAEADPSRSTEWLRP PHHSSDCLRGLAHIVSQWVSEC LLCSPGSPPRSPLWALCWEHWE TWPALPEGNQSPPEGLPPCSRS QWPQTPPASDPQ
28274	58642	A	28446	3	213	LTQHCWTHLVRSSHSRTGSSRL HNHQLHQPAC*SLCQKEHASR GWSEGFNLWRNKK**C*DKKH KTAG

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28275	58643	A	28447	142	772	LVNVVDVADLVGLCVSHRHVT EEQYSTLALLNHGPQVALKYV HMDEVMPACCLEGGCLPAL CGECKLQGSFILSAPGRQGSQR VGPREAQGHVIGRKLFFSTALM LIGGQRLEESAAIESGCMETP QGMAGSPQVGQAQKSPSPVNPKE PIGDF*GGSQDYRGGIQKPID*Q CGPVI/SRQSELWCGGRSHSVE FLLGSAASAPPGPQA
28276	58644	A	28448	1	1935	
28277	58645	A	28449	2	1571	
28278	58646	A	28450	2	301	PRPFYSKNFYKILSYSSSEFNNS FVDA/LGSD/QDSGNEVDVDM YTEAAEELKRNAEVIVFIPEYS WSNSVSLFPLCPGAKGPTFSVH CRVHFGPFSSH
28279	58647	A	28451	1	1329	
28280	58648	A	28452	240	503	
28281	58649	A	28453	1039	1896	
28282	58650	A	28454	1	2397	
28283	58651	A	28455	1	4011	
28284	58652	A	28456	3	1088	
28285	58653	A	28457	1	4878	
28286	58654	A	28458	1	174	
28287	58655	A	28459	3	161	
28288	58656	A	28460	992	1102	
28289	58657	A	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV GFPOGQCLVHIW*/M/PLDAGPE HNSLKGFLVPLFPLAATPRAPG TPAQGSLTDSFPDLLGLAAED
28290	58658	A	28462	3	278	HEAAMSMLRLQKRLASSVLRC GKKKVWVRPL*/TNEIANANSR QKIRKLKLDGLNRTFVTAHSWP SCRNTLSRRMGHS*/SLRTLDD PVNM*GLLNASWITKC*LLDPV NM
28291	58659	A	28463	1	1043	
28292	58660	A	28464	185	804	VTSGCGKKKVVWLDPNETNEI ANANSRQQIPEASSKMGLIRK PVTVHHSRA/RCPVKTP/LARRG RGRATWGIR*/GGKGYKPNARN AQRKFTWMRENGGL*/TRGCL RKIPVNPCKDRIANMYHSLPLE G*RGNVFKNKADFSWEHIHKL EGRQRPRKKAPWLTAQ*/GPAG S*/DPRKPKRR*/RAPRPPKKEI HQRLFSKE/EETKK
28293	58661	A	28465	221	350	GPSSFRLPTLSSLVHSHGREET* HSLET*/RDAVSLRIFKSLSV

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28294	58662	A	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQGNKRGYKQME EHSMLMGRKNQYRENGHTAQ GNLQVHAIPIKLPMTFFTELEKT TSKFIWNQKRARITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKLK SFCTAKETTIRVNRQPKKWEKI FATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAHQKSG NNRCWRGCGEIGTLLHCWWD CKLVPHILTHRWELNNEITWTQ EGEYHTLGTVVGWGEGGGIAL GDIPNAR
28295	58663	A	28467	1	1863	
28296	58664	A	28468	2	1308	

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28297	58665	A	28469	1	1901	MPESPTLLGRDILAKAGAIHL NIGEGTPVCCPL.LKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFYQQRQYPLRPEAQQLGQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNQWRLVQDLRIIDE AIVPLYPAPNPYTLSSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPPQ FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQEQECHQATQV LLNVLATCGYKYSKQAKLCS QQVKYLGVKLSKGRALNNEE QIEHNCQQVIAQTYATRGLLE VPLTDPNLSLYTDGSSFVEKGL QKGGYAVVSDNGILERNLTPG TSAQLVELIALPRALELGEGKR GSSESICFLSFLVPPMTIYTEQDL YNHVVPKPRNKRVPILTFVVGA GGLGGLGTGIGGITTSTQFYFK LSQELNGDMEWVADSLVTLQD QLNSLVAVVLQNRRLDLLTA KRGGTCLFLGEECCYYVNSQGI VTEKVKEIRDQIQRRAEEI.QNT GPWGLVSQWMPWILPFLGPLA AIIILLFLFGPCIFNLLVKFVSKI EAVKLQIILQMPEQMMSMT/KI YHGPLDQPASPCSDVNDIKGTP PEEISTAQHLLCPNSAGSS
28298	58666	A	28470	1	432	
28299	58667	A	28471	1	4314	
28300	58668	A	28472	1	330	
28301	58669	A	28473	1	1425	
28302	58670	A	28474	3	1110	NEEQIEHNCQQVIAQTYATRGD LLEVLPTDPNLSLYTDGSSFVE KGLQKGGYAVVSDNGILERNP LTPGTSAQLVELIALPRALELGE GKRGSSESICFLSFLVPPMTIYT EQDLYNHVVPKPRNKRVPILTF VVGAGGLGGLGTGIGGITTSTQ FYYKLSQELNGDMEWVADSLV TLQDQLNSLVAVVLQNRRLD LLTAKRGGTCLFLGEECCYYV NQSIVTEKVKEIRDQIQRRAEE LQNTGPWGLVSQWMPWILPFL GPLAAIILLFLFGPCIFNLLVKFV SSKIEAVKLQIILQMPEQMMSMT TKIYRGSLDQPASPCSDVNDIEG TPPEEISNAQPLLCPN*AGSSWS SRRPTSPALGFSC
28303	58671	B	28475	1	1989	

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28304	58672	A	28476	1	1280	MGNITADNSSMSCTIDHTIHQT LAPVVYVTVLVVGFPPANCLSL YFGYLQIKARNELGVYLCNLT ADLFYICSLPFWLQYVLQHDN WSHGDLSQVCGILLYENIYIS VGFLCCISVDRLAVAHPPFRFH QFRTLKAAVGVSVVIWAKELL TSIYFLMHVEEVIDENQHRVCF EHYPIQAWQRINYYRFLVGFL FPICLLASYQGILRAVRSHGT QKSRKDQIQRLVLTVVIFLACF LPYHVLLLVRRYWEASCDFAK GVFNAYHFSLLTTSFNCVADPV LYCFVSETTHRDRLARLGACLA FLTCSRTGRAREAYPLGAPEAS GKSGAQEEVTKFEGGRNGHT AKKSPCNSVQDFTGIKAVKLQI VLQMEPQMOS/KLKIYSRPLDR PASPCSDVNDIEGTPPEEISTAQ
28305	58673	A	28477	1	717	
28306	58674	A	28478	2	409	
28307	58675	A	28479	1	675	
28308	58676	A	28480	227	399	
28309	58677	A	28481	332	436	
28310	58678	A	28482	980	1399	
28311	58679	A	28483	132	218	RINLMHFRN*TSQQALSLSYNL FLMQRH
28312	58680	A	28484	1	34	
28313	58681	A	28485	985	1170	
28314	58682	A	28486	1	1203	
28315	58683	A	28487	505	716	REPCVPSQREVWRPGCLD/HCP RQSGSLGETLRGTAEQPWPHS QVLSNLRVLQLPLISPLRRRA LFPA
28316	58684	A	28488	1	998	
28317	58685	A	28489	477	955	TPIHNGFKENKIPRNPYKGC EGLQGEQTAEAGNKRGYKQM EEHSMMLMGRKNQYRENGHTA QGNLQVQCHPHQATNDFLHRI GKNYFKVHMEPKKSPHRQVNP KPKEQSWRHHIT* ¹ LQYYTTRL Q*PK*HGTGKTKEI*INGTEQSP QK*CRISTTI
28318	58686	A	28490	37	430	
28319	58687	A	28491	507	829	
28320	58688	A	28492	643	945	CALLHSLPQHCVQHPYRSYTHR MASCRWKWGHCHSGIKMYSIP WYSTPMEGKALGDAHPQIAHS H*GAFL*ALY*EKS*SMANRL WYSRL*PLAGDGRRE
28321	58689	A	28493	1092	1346	

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28322	58690	A	28494	173	527	
28323	58691	A	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSPVSPALPCSLKYPFYD HRTKFTLTTPQFSHTLAQKENQ SPLKHMGGKKRLQNIFLPIRP*DQ TPWLEERS
28325	58693	A	28498	921	1008	
28326	58694	B	28499	1	2169	
28327	58695	A	28500	455	523	YPLYHFLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVYSEIQLLPGLVL GGCMCRGIYPFLDLFLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLLRVFSMKSC *ILSKAFASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFASILLRIFTS MFIRDIGLKFSFFVVSLLPGFGIK MMLAS
28330	58698	A	28503	1	957	
28331	58699	A	28504	41	412	IALIILRYIPSILLRVFSMKGC* ILSEAIASIEIIMWFLSLVLF*W ITFIDLHVLNKPICPGMKPS*SW WISFLMCC*WIFASILLRIFASM FIRDIGLKFSFFVVSLLPGFGIRM MLAS

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28332	58700	A	28505	1	1699	MDEFLDITYTLPRLNQEEIESLN RPITSSEIEAVINSLPTKKCPGPD GFTAEFYQRYKEELVPILLKLIQ TIEKEGLLPNSFYEATNIIIPKPG RDTTKKENFRPISLMNINAKILN EILATESSIKKLIHHDDQDSFPGM QGWFNICKSINVIIHINRINKN HMIISVNAEKAFAKDRIHFLMLK TLIKLGIDETSLKTVRAIYDKPT ANIHLNGQKLEAFPLKTGIRQGC LLSSLLFNIVLEVLAIRAIQEKEI KDIQIGREEVKLSLFADDMIVY FKNPIVSAQNLLKLGNSFSKVS YKINVQKLQAFLYTNNRQTESQ IVSELPTIAAKRIKYLGIQLTRD VKYLFKENYKPLHKEIIEDTNK WKNIPCSWIGRINIMKMAILPK VIYRFNASPIKLLNFFTELEKN CLNFIWNQKRAHIAKTILSKKN KAGGITLPDFKLYYKSTVTKTT WYWYQNRVIDQWNRTEASEIT PHIYNHLIFDESDDKNQWGKDS LHNKWWYENWLAICRKLKLD SFLTHYTKINSRWIKDLNAGSKI QYHADRTKSRERRAIASSYVSS
28333	58701	A	28506	2	1689	WRAWGRGATRRESSCHRQSAPS LSRVGRSSQIRSAASAASGLWR RKPAKAFGRPRTGSLHLVPK* KAFVSLQESSA*MNLRO*PE*D WISWIN*QNFQN/CQGSTLKIPV VERKILDLIALSKHSFSPATEQ SWTENDFDELREEGFRSDSE LKEEVTRTHRKEAKNLVVKRLDK WLNRTSVEKSLNDLMELKTM AREQLRDECTSFSSQFDHLEER KYKLPSENKHYANKLENLEE MDKFLETYTLPRLNQEEVESLN RPITGSEIEAIINSLPTKNSPGPD RFTAKFYQMYKEELVPFFLKLF QSIEQEGILPNSFYEASIIIPKPG RDPITKKENFRPISLMNIDAKIFN KILANQIQHKKLIHHDDQMGFI PGMQDWFNIRKSINVIIHINRT KDKNHTIISIDA EKAFAFDKIQQCF MLKTLNKLIGDGTYYKIRAIY DKPTANIILDGQKLEAFPLKTST IQGCPLSPLFNIVLEVLAIRAVR QEKEIKGIQSGKEEVKLSLFAD DMTVYLENPIISAQNLLKLSN FSKVSQYKINVQKSAFLYTN
28334	58702	A	28507	1	1428	

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28335	58703	A	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC WIMFIDLRMLNQPTPGMKPT* SWWISFLMCCWIRFASILLRIFA SMFIRDIGLKFSFFVVSPLPGFGIR MMLTS
28336	58704	A	28509	765	950	LLPQFQNLLLVYSEIQLPLGLVL GGCMCPGIYPFLDLFLVYLHRG VYSIL*W*FVFLWDQW
28337	58705	A	28510	778	981	SQKEWYQLLFVPLVEFGCESIW SWAFFGWQAINYCLNFRITCHW SIQRFNFFLV*SWEGVCVQEFIH FF
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI* TLK
28339	58707	A	28512	1	1641	
28340	58708	A	28513	1	2307	
28341	58709	A	28514	1	3793	
28342	58710	A	28515	178	674	ERPRIMDLAAGLLKSQFLCHLVF CYVFIASGLIINTIQLFTLLWPI NKQLFRKINCLSYCISSQLVM LLEWWSGTECTIFTDPRAYSS MGKENAIVLNLHKFGN/DFLC GWSLSERFGLLVGSQKCIPLCL THFFGSAPPLVFLLLVIQNLQKN QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCGLFFGSI* TLKYFFPIL
28344	58712	A	28517	1	2167	
28345	58713	B	28518	65	2652	
28346	58714	A	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	A	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	1	669	
28351	58719	A	28524	1	1089	
28352	58720	A	28525	91	507	AGTASASPAPNRSLSGSEPTSS VTQENGADVQGHervVPWKKAR SRRFCPMEGTRKVPVSHGSHVP EVSMLWKACSGSFRPVEGHVS RCALTASGCSPP*AGTASASPAP NRSLSGSEPTSSSVTQENGADV QGHervVPWKKARSRRFCPMEGT FRKVPVSHGSHVPEVSMLWKAC SGSFRPVEGHVSRCALTASGCS SPSKSKATVGCRCSDFTVEEF LQKIFLQVESLDRRRCLPLT
28353	58721	A	28526	1	1213	
28354	58722	A	28527	130	211	KPHYAAHGQPFAT*RPGETDNR ADNRQ

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28355	58723	A	28528	793	1382	NTTAAGRIVRLTSENGSHTTFR YDVLDRLIQETGDFDGRTRQRYH HDLTGKLRSEDEGLVTHWHY DEADRLTHTRVKGETAERWQY DERGWLTDISHISEGHRVAVHY RYDEKGRLTGERQTVHHPQTE ALLWQHETRHAYNAQGLANR CIPDSLPAVEWLTYGSGYLAG MKLGDTPLV**ERPADR*ASDG ASPADGSTALAA*DQTCVQRA GAGEPLYTGQPARRGMADLRQ RLPGRHETRRHTAGGVHPRPPA PGNAAQLRPL
28356	58724	A	28529	1039	1689	
28357	58725	A	28530	1	2406	
28358	58726	A	28531	1	2928	
28359	58727	A	28532	2	1271	
28360	58728	A	28533	250	929	
28361	58729	A	28534	3	273	GKLIIVIGDEDVTGFLGIG ELNKNRHPNPLVVEKDDTTINEIE DTFRQFLNRDDIGAFLRLGLCW LRNRKPDHLPPLPCA VTQCH
28362	58730	A	28535	2	415	
28363	58731	A	28536	1	690	
28364	58732	A	28537	2551	2651	
28365	58733	A	28538	2	295	
28366	58734	A	28539	1	316	CGHGGRQSWVSLR* CQEAAG MADSCPRSGGAILAFKSAPEVI RRALSAQSLRATSSSSASGAGA FCLSPSKYFETSASSSATARYV LGWAASSGLLTSSQKMG
28367	58735	A	28540	1	400	
28368	58736	A	28541	257	516	
28369	58737	A	28542	1	590	EQIASDTHLQRVVFKNISPAD AHRNLCLALRGHKTVTYTLTQ GNDQDDMPALCEVLRHPECN LRYLGLVSCSATTQQWADLSL ALEVNQSLTCVNLSDNELLG*G C*YAVHN/*DTPSAFLQRVVV GKTGHLTEANLQGTLLLCWVF SRELTHLCLAKNPVNTGVKYL CEGLRYPECKLQTLVLWNCIT
28370	58738	A	28543	1	2633	
28371	58739	A	28545	127	2030	
28372	58740	A	28546	1	3066	
28373	58741	A	28547	259	3222	
28374	58742	B	28548	1	2640	

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28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADQRLIF AKSWPRASRYQQGHQDLFILRS DLPSQVVQTQNISSCRNRC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QK\SDGTLQEHDGICEIHVAKY AEIFGLTSAEPNRFQTQRLSETK EITNPFYAMRLYESLCQYRKPDG SGIVSLKIDWIIERYQLPQSYQR TSPCCCHMKKDVFASTMISS SRVSNNTSKTTIKNQCQKDDSD RRSLLVKNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGVVR RCLQQQCEQTVRILHAKVAQK SYGNEKRLIIRPTIRVGPWSQTN NQTDSTSGTVVQSDYQTDSDTS GTVVRTNNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	B	28551	1	1954	

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28378	58746	A	28552	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAFA KENNQKAYKETYGVSHTHRD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGPS KDADDTSIYMFYQKVGDNIDS WKNAGRNVFKDSKDFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHGKQSLTTAQVNV SKSDDTLKINGVEDHKTFIDGD GKTYQNVQQFIDEQNYTGDPL EAETA VINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAESKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIERYQLPQSYQRT PDFRRRFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIIKAWIERY QPPQSYQRMPPDFRRRFLQSRPA CMHDWLCAEALWSIQTASYL VTMQVNLTSLSSDTRDLSSVS NSGWVSSGSLVRFNTIKTSSEGEI KRTVPRLPDPDDPRSAIAEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLI.PKAVHLA
28379	58747	A	28553	2372	3570	EALLPGDQDSQSGKGVAAAREV WFLPSSFAPVLLRLVGNHHVG DNSIDSWKNAGR/VFKDSKDFD ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHGKQSLTT AQVNVSKSDDTLKINGVEDHK TIFDGDGKTYQNVQQFIDEQNY TSGDNHTRLRDPHYVEDKGHKY LVFEANTGTENG YQGEESLFNK A Y Y G G G T N F F R K E S Q K L Q Q S A K K R D A E L A N G A L G I E L N N D Y T L K K V M K P L I T S N T V T D E I
28380	58748	B	28554	I	2232	
28381	58749	B	28555	200	2602	
28382	58750	B	28556	I	3198	
28383	58751	A	28557	I	2169	
28384	58752	A	28558	I	2259	
28385	58753	A	28559	I	2418	
28386	58754	B	28560	I	1974	

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28387	58755	A	28561	3	2077	
28388	58756	A	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETVGS HITRHDMLQIPKQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDSIYMFYQKVGD NSIDSWKNAGR VF KDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKT FDGDGKTYQNVQQFIDEGNEGI LPISPEPIKQDFRLLG
28389	58757	A	28563	610	2303	SLPNLDNAICSSSSPTRTR*SL SEGATQAFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDSIYMFY QKVGDNSIDSWKNAGR VF KD DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHLLRDPHYVEDK GHKYRGPLESPSTHQEFNPTS CVSSLGTLQGFPAWLAALAH VHPLKHKSGGSNRLSAAIWGIK RKPARVCPGTGIHASSQIQGEW RTECAVGP KAKAKATAGWRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQTY ESIVDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEVDVRI LLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVKGQIR MRTVFEQAIDQRSSTGAWRNA LSIWEPCNEIFDRILKPRWEIR
28390	58758	A	28564	1	2079	
28391	58759	A	28565	1	774	

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28392	58760	A	28566	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDDTSIYMFFKR GAIFRVHKHAVNPMSPKCRPPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKETYPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKADDDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYSNDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQSAKKRDAEL ANGALGIIELNNDYTLKVKVMKP LITSNTVTDEIERANVFKMNGK WYLFDTSRGSKMTIDGINSNDI YMLGYVNSLTGPYKPLNTTG LVLQMGGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ MNNASTMSKRTSAGCHCWQG
28393	58761	A	28567	1	3987	

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28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNAAGR/VFKDSD KFDANDPILKQDTQEWGSGATF TSDGKIRLPHYTGSLSNKKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNAAGR/VFKDSD KFDANDPILKQDTQEWGSGATF TSDGKIRLPHYTDSYSGKHGKQS LTTAQVNVKSDDTLKINGVED HKTIFDGDGKTYQNVQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL/VFEANTGTEHPQPQ/ERP RTQSFSAFAERECIPNVPADT KLSKIKTLRLATSIAIYLMDDL AKDDQNGEAEAFKAEIKKTDV KEEKRRKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAAPPPTHMEGFEL FHL.PDLCSPSQDAQTITGRQMKG PDHSPRPSHRVPQAKGNNVVIT SYMNTNRGFFEDKKATFAPFLM NIKNKNTSVVKNISILEQGLTV
28395	58763	A	28569	2	1778	
28396	58764	A	28570	1099	2224	DGQQLIALHRLALRELQQA V H AGLPQQA KILFDGGSE/TRQNPL QQLVHMG LPRPLDKKNFQEP
28397	58765	B	28571	1	1938	
28398	58766	A	28572	1	2367	
28399	58767	A	28573	4659	13369	TVFRPFHVGVHLLIVDSCSKL EQHSTLSRAILLIYKGCFRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTGKRAVSATQLMDFADFGT TIKQDFRL LGQTSVDRLLQLSQ GQAVKGNQLLPVSI.VKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGGGEDSPNRRFFDGG RKKQIRTVRQFIDEGNNTPADT QTLRDPHYVEDKGHKY
28400	58768	A	28574	6803	8521	
28401	58769	B	28575	2010	17745	
28402	58770	A	28576	1	1060	

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28403	58771	A	28577	1	3585	
28404	58772	A	28578	44	317	LKALLLTQSLFGGLLTQTRMKF GAVTRIGDLPWEINPLSSCSLL HEKDPPTTSGPQTHQPKHELTN FKSGCSPCRAKSQFFLSLCSST
28405	58773	A	28579	98	617	KALLLTQSLFGGLFTTRMKFG AVTQIGDLPWEINPLSSCSLR EKDPPTTSGPQTHQPKHELTNF KSARFKKIKACYHSPATAWPFK AYKLSLQFPHTCPKTRQALQV SSGSVPYQPNCFAYPPHGAKPI YSPILNTSLHNPLFCSGSQTCFL YYSFAPFIPASLRFHLD
28406	58774	A	28580	1	1500	
28407	58775	A	28581	42	257	
28408	58776	A	28582	3	425	KTGKYD/AVIALGTVIRGGTAH FEYVAGGAS/NTLAHVA/QDSEI PGAFGVLT/LKA*TNDEAGTKL HGGWGGKCLTACRSALWADL QIRPYDHKNRGSNVHNRVPAS GAAAMAHCLECGWAPLAAGD NVGKVCVPDAGLLPA
28409	58777	A	28583	327	1512	SYWTIHQVSLINHSYLPGGIS SLKKMAGRNSEKTVLVKSSF QEVNRGTEALALWENGDFEAP VLTFTTALLPEGATQAFGKENT QKASKERYGSLNITRNMLQIL NKQQTEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNIDSWKNA GRVFKDSDKFDANDPILKDQQT EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHILRDP HYVEDKGHKYLVFEANTGTEN GYGGGVNADVGDVVVRLPVW HRRGGEAVFMQVSRQLRLHLP HGVAVDRDHHIAHRRRHVA GDRSGSVRL
28410	58778	A	28584	845	966	
28411	58779	A	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIACTGHIDP VTRFRPRAR*GSSHRNKAVDTR RH
28412	58780	A	28586	464	847	

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28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ GIKRPDALPGPLLHA*PDNLRCSPRSGTAAGSIHQDARLRYSVWRWGLLDRLAAVICRQSTHSRCRRKQRRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	A	28589	404	733	
28416	58784	A	28590	2	246	
28417	58785	A	28591	466	861	
28418	58786	A	28592	122	926	
28419	58787	A	28593	171	733	
28420	58788	A	28594	1	774	
28421	58789	A	28595	1	1575	
28422	58790	A	28596	1	105	SVKLGWNGVSTYVPFCLTICSV SFFQENLHLTTCRA*PSIPPPAARRSPKKCS*KLRLP*LSGSSS YNL
28423	58791	A	28597	237	461	
28424	58792	A	28598	1	1341	
28425	58793	A	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGLFPRKSSSRHRGKVKSF KDDPSKPVHLTAFLGYKAGMT HIVREVDPRPGSVNKKVEVEA VTIVETPPMVVGVIGYVETPR GLRTFKTVFAEHISDE/CRLLPL RQKKAHLMEIHVNGGTVAEKL DWARERLEQQVPVNPVFGQDE
28427	58795	A	28601	1	1251	
28428	58796	A	28602	37	1307	EFGFDGVMSHRKFSAPRHGSLG FLPRKSSSRHRGKVKSFPPKDDP SKPVHLTAFLGYKAGMTHIVRE VDR/PGIHRCNKKERWWRAVT HCIRPPMVVGGHLVGYVETVP RGLRTFKTVFAEHISDECKRRF YKNWHKA/KKKAFTKYCKKRQ DEDGKKQLEKDFSSMKK/YCQ VNRVIAHTQ/MRLPL/RQKKA HLMIEQVINGGTVA/EKLDWA REKLE/QQ/VPVN/QVFGQDEM DVIGGDQRAKGFQGVTR/WPT N*L/PFKA/HGL/SRVACFGAW HPARVAFSVARAGQKGYHHRT EINKKIYKIGQGYLIKDGKLIK NASTDYDLSDKSINPLGGFVHY GEVTNDFVMLKGCVVGTKKR VLTLRKLLVQTKRRALEKIDL KFDITTSKFGHGRFQTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	A	28603	1	2133	
28430	58798	A	28604	3	245	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
28431	58799	A	28605	1	1824	
28432	58800	A	28606	1	1035	
28433	58801	A	28607	1	496	
28434	58802	A	28608	1568	1793	
28435	58803	A	28609	1	1392	
28436	58804	A	28610	1	1389	
28437	58805	C	28611	104	253	
28438	58806	A	28612	114	469	VSRPTYAKVFVTSKTAPOKVFPTA WCSA/TGHETALSA/TQVPIQWIATAPNSPAPSPDPRRQSWVSQIPSSATSPNFTM*EPRTIQEVTEPHDSRPAIPSAVPRRESCTGRPHLPATTP
28439	58807	A	28613	3	2196	
28440	58808	A	28614	237	348	NPVN*SQTT*TSE
28441	58809	A	28615	950	1094	
28442	58810	A	28616	146	822	LGFLRLRLSEMPRKQGVYRTRIRWKFEDGLSNVLVI/PIEQINHMMDVFGSGSERATCLARGGYINSLARCQNLVNRDL/DHLSLPQDSTLVHYIDIVLVHGFSEEKGGQVAQSADL/DEGLLKIPGDTFGPEADKDFLHKDLSTEIVGQSYNTHHMAQDSIPWNPSPQEPQVREHEACHHLGSGSPSPWELCEQGPVTESFQVLVTSGLDKENMAYMHCGIICSNNKKG
28443	58811	A	28617	1	1791	
28444	58812	A	28618	244	416	
28445	58813	A	28619	2	1520	
28446	58814	A	28620	95	421	PVTSTSTKRTPTQKPHPKVISLKDQIHVV/DKSMRMKNQCKNV ESKSNQNSSPHDHNSP/SARAENWTEYESDKLTEVGRGWVINSSELKEHVLTHCKEAQNLHN
28447	58815	C	28621	46	174	
28448	58816	A	28622	425	1291	
28449	58817	A	28623	1	1410	
28450	58818	A	28624	14	348	GLFPNKPFSVLEIRTWAHLSGRHHSACHTSCAWPQVACLPLATHPSCTCTFCSLQAPGRPGQSPLSPRRACGPEDLPPPPYV*DLAPSLGPSLGLPLMSQSQPRRTPLRG
28451	58819	A	28625	96	295	PWKPHPAWRQRWELCHPPFP/I RPLTAALREQGLLGRSTTVFTLMAREPPQAAADSLCIVQME A

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28452	58820	A	28626	105	389	CQFAHGTASSPRVCLRHRCRS WQKAWAVVCCITFCSLQAPGRP GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQPRRT PPLAWGS
28453	58821	A	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	A	28629	301	987	
28456	58824	A	28630	239	384	VLPAGAAQAARSSDTRP*PEPH FSVESVFPRWIFSFAQLNNFFQARF
28457	58825	A	28631	1	1054	
28458	58826	C	28632	243	392	
28459	58827	A	28633	1	1104	
28460	58828	A	28634	194	863	YLLFVKNMSSLEISSCSFLETK LPLSPPLVEDSAFEPSPKDMDE VEEKSKDVINFIAEKLSDVEVS QLVISPLCGAIS/LNWKGLTENT FEGKKVISLIEYAYLPMANE VRKICSDIRQKWPVKHIAVFHR LGLVPVSEAKP*SFAVSSAHRA AISLKLSSYC/AEDTFKRPRVPI WKKIEIYESSTWKGKNECFW ASNTLITYVFRACNLNFVKLL
28461	58829	A	28635	3	338	SSPPTAPAKLRIVPLVGGLPAR WCLSVCAQCQPDTRVHVFHLHW WCSSLCPAPVCLSLCRGL*GHF PPDSEDQSSPNCSGYTLEEKYKL LRSQTIPSCNGKFPCCPRRAYDG
28462	58830	A	28636	405	800	
28463	58831	A	28637	265	539	
28464	58832	A	28638	3	1116	
28465	58833	A	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	A	28641	563	594	
28467	58835	A	28642	245	580	
28468	58836	B	28643	1	435	
28469	58837	A	28644	673	1012	QPQVSFSSEYAIHMRCPHSKIS SLYYFNCFRY*DCYCHVIFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLTGA WVRAWKATSTSVVHLTKWVL
28470	58838	A	28645	1171	1328	MVIGGTKNERKHIDSEPLFPSP NSSARGRAISST*ALVPGVRGF LSSIPLSLTTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGSVDLSHGLHLGLHL KNDL*FYFNSGIDKPEIAKLSG CSFGGTFLLIWG
28472	58840	C	28647	199	309	

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28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLPLKLL L*SYKSFFKWSRCS
28474	58842	B	28649	107	264	
28475	58843	A	28650	301	470	EIQVLVLSGGGYSHAVLMIVS SHKI**FYKGLFPTFALHFSLLP CEEGCICFPF
28476	58844	A	28651	2	263	WEKKDTEWRKKVILSSV*LRL VIF**PFSMLMLFSPVWR*ARSH ESHLAITHLWALYF*PPCQICFL *DRGHQATDGLTNGTPSELN
28477	58845	A	28652	63	191	DLPWTPGPAC*PMLQC**GGAN IYARRQGADAAGDQGSCL
28478	58846	A	28653	1	554	MPTYCPGASLLITYKTPKELLS IYVSTIRKSRERRRRLGAR NFRSEEQIYDQWRDLQVGKFFP FPRPRENYHFGSEHVGSFSLDK CCNEKLYEVIDLHLKKFLNTE TSLSLVKCEVSRCWVTLNLLLPY H/VLFQI*LSWRERQNSCKTTN GSSNGAPDAVHN*NLLWSLGP AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWPALPEN GYMKQFCVSGLGVLFHGCVFL CWHHCCFVL*VWSLGSPPSRG LHLVKAFFLCYPRSNCFLLNWG IVGVQRLRFQEGCLWCH
28480	58848	B	28655	1	400	
28481	58849	B	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTALPVSSQPSLHTA EVQGCAGVILTQGPQCPVAF SKQLDLTVLGSPLHAVAASAA LILLEALKITNYAQLTYSSHNF QNLFSFSLTHLSAPRLQLYS LFVESPTITLPGPDFNLASHILD TTPDDDCMSLIYLTFTPFPHISF FSVPHVDHIIWFTDGSSTRPDRH SPAKAGYAESSTSIIEATLPPS TTSQQAEIALTRAFTLAKGLH VNIYTDSKYAFHILHHHVIWA ERGLT/IARVLHH*CLFNKNSS QGCFSTKGSWSHTLQGPCKGV RSHYSRKCLC
28483	58851	A	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	A	28661	1	704	
28487	58855	A	28662	41	275	
28488	58856	A	28663	159	1504	
28489	58857	A	28664	275	552	
28490	58858	A	28665	178	619	
28491	58859	A	28666	3	369	

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28492	58860	A	28667	1	340	
28493	58861	A	28668	516	734	WTGDWRRRTCDRENQHVSGAA RTAFIPTNGAISPGINYSFGH*Y* DCHLPQA*P*LCRAAGQNRCH VARTCLG
28494	58862	A	28669	1	1163	MHTHARETCLALGKPADDATL TAAIEAVGLENAARVLKLYPFE MSGGMLQRMAMIAMVLCESPF IIADEPTTDLDVVAQARILDLLE SIMQKQAPGMLLVTHDMDKW GRIIADVESQYRYQTNPKEIFAG GDVARGADLVVTAMAEGRHA AQGIIDWGLDVKLGAELEERR KVLQVKTENLQAERNRSRKSIG QAKARGEDIEPLRLVKNLGE LDAAKAELDALQAEIRDIALTIP NLPADEVVPGKDENDNVESVR WGTPREFDFEVRDHVTLGEMH SGLDFAAA VKLTGSRFVVMKG QIARMHRALSQFMLDLHTEQH GYSENYVPLYVNQDTLYGVGL YPLGALASGW/WALASGWLPK RRERKD/GDTGAHGVPRGSRKP RIARKVRGT
28495	58863	B	28670	1	4770	
28496	58864	A	28671	1069	1398	VIGAQPVLIRRRKQARRQINRL TLILLHYCLTTKLKNVKGPIV AAFYFLPGAG*IHPAGCHGTQL *SFGKMRVQYTRVTLSQQASG KISAYLIDLKGKLLKLIHCGVH
28497	58865	A	28672	4246	4453	
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	A	28675	1085	1246	
28501	58869	A	28676	1	1254	
28502	58870	A	28677	1	2175	
28503	58871	A	28678	340	994	
28504	58872	A	28679	37	261	TITPAGRRMHCKGACMKPLLD VLMILDAVRELE*TITPAGRRM HCKGACMKPLLDVLMILDAVR ELEKQAIKLHEGWENELVIGVD DTFPFSLAPLIEAFYQHHSVTR
28505	58873	A	28680	410	896	WAWAASAVQPRSIWQ/GAGVG NLTLDFDTVSLNLRQTLHS DATVGGPKVESARDAPHIAITP VNALLDDAELALIAEHDVL D/WYG*RCGT*STERQR*RG* RSAPAMTAHDRDAJASSETCA RSRWSVEYASPCAPPDSRSKR RSASNSAASHVF
28506	58874	B	28681	1	2298	

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28507	58875	A	28682	1915	5313	
28508	58876	A	28683	1	4221	
28509	58877	A	28684	1	1007	MAALQMVNGQKQWVSSNQKY WLVYKTTDPRLRPFGVQPM CPFNGRPFVHKNPMPGVHWAV ATGLALIPVIGAEFGWFVFGG ETYMMAWNVSGLGTGAIQST FNVTLWSFIGVESASVAGVVK NPKRNVPIATIGGVLIAAVCYV LSTTAIMGMPNAAALRVASPF GDAARMALGDTAGAIVSFCAA AGCLGSLGGWTLLAGQTKAAA ADDGLFPPIFARVKNKAGTPVA GLIIVGILMTIFQLSSISPATKE FGLVSSSVIFTLVPYLYTCAAL LLLGHGHFGKARPAYLAVTTIA FLYCIWAVYITHIDACVVVYIA GYRAAKLTCA
28510	58878	A	28685	867	1681	
28511	58879	A	28686	865	1290	RWENRRLFRKNPARAQKMLV PERFG*SAYPNGFAGTWRLDKL PIAQIHAHMIGYLAADVMEKQ QISPAQVVRVHRNRCPIAIVHLI GRARELSLKD.VVGKKNQPATV KAFIRPTAPDVLAKLLQAV NRHFGNVQMVA
28512	58880	A	28687	1	709	
28513	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPQT AFIQVGPVRVHAHLQPRAPL*A GEVWKPRLVGRSHWASRPSA LQKGEPGSPSWENACVPQAPH RLLHQKAF
28514	58882	A	28689	3	227	NSQDFPACGGGLCHAEELRTAA GLVHQVHRPHGTSVAAEKLCH GDVEGDGCNGPASD/PGYI*GQ AAAPAPLPDLL
28515	58883	A	28690	1227	1719	
28516	58884	A	28691	1	1701	
28517	58885	A	28692	15	3298	
28518	58886	A	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR AVWRYQTDIAANLE*RRLPSCA GKSDWSSGDSEKAKTAAHTIY RDAGRRVRGYRQL
28519	58887	A	28694	1	370	

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28520	58888	A	28695	1	910	MDKERIIQEFVPGKQVTLAHLI AHPGEELAKKIGVPDAGAIGIM TLTPGETAMIAAGDLALKAADV HIGFLDRFSGALVIYSGNYTL ARKTQAVEFNDKGDIDTPGEYF NHPRWYHALITTLQDQDMLSP LIWGFERNYKDVQVIKATPHKIV ILMGILLSPSVFATDINVEFTAT VKATTCTNITLTGNNVTNDGNN NYTLRIPKMGDLKIANKTTESQ ADFKLV\MGAAVASVGLIPL* PEMHQAHLISLLYRSLVIHLRR QVISVWVSKNGLLMMPLSLNL TVRKRYAGAQTCSPIRVLK
28521	58889	A	28696	605	2021	
28522	58890	A	28697	2256	2336	CIKCCARRIAREPGYLF**RCK YPG
28523	58891	A	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN V*SWIKSS/MQMGQKMGVKISD EQLDQAIAIANAKQNNMTLDQM RSRLAYDGLNYNTYRNQIRKE MIIEVRNNEVRRRITILPQEVES LAQQVGNQNDASTELNLSHLI PLPENPTSDQVNEAESQARAIV DQARNGADFGKLAIAHSADQQ ALNGGQMGWGRIHASLPGIFA QALSTAKKGDIVGPISGGRFD GTVEVKDGLHIVNGKKIRVTAE RDPANLKWDEVGVDVVAEAT GLFLTDEETARKHITADTPAALR WLEENQLEDGHECLLRVVISSD GRSRGFINGTAVPLSQLRETSTT TGARRVIRAIRINSSDASTIPTL MAITISNNTVSDMHSSMTMMS TRIRTLITTYNGDLRMIRQRKL CKTAIARTYGNDDTFHPGMRH QRMHIRVFNAPILDDQPVVTLN IYPKADESSSLKASRGTRGAAY RPARQNLYSASSGKKDENPVIE FKNVSKHFGPTQVLHNIDLNIA QGEVVVHIGPSGSGKSTLLRCIN KLEEFTSGDLIVDGLKVNDPKV DERLIRQEAQMVVFQGFYLFPHL TALENVMFGPLRVRGANKEEA EKLAARELLAKVGLAERAHHP SELSGGQQQRVAIARTLAVKH KMMLFDETTDFDPVLVHEVL KVIHEFAEKGITNDSLTENPAKT QGEQGCLQSQERGQPREPTPRH
28524	58892	A	28699	1	2307	
28525	58893	A	28700	3	976	

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28526	58894	A	28701	2	136	YLSAV*FCSPGQPPSALLVCGR RGYWCLWPLSSCHLLRLRLCVS
28527	58895	A	28702	1	608	
28528	58896	A	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	A	28705	1	1184	
28531	58899	A	28706	478	627	
28532	58900	A	28707	33	1072	
28533	58901	A	28708	35	516	RVVEFADEGQGPAALSLWSGS SPETLKLHWPVHQ*IRFSSWK TFRIRSRDFWADRLMRTLRLNRF LSKWDHL*QTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRDDGLAGLRGN SGAQGGDA
28534	58902	A	28709	1	777	
28535	58903	A	28710	531	704	
28536	58904	A	28711	294	617	
28537	58905	A	28712	804	1020	HFLSGGRRQRPPRWITVA*SPR* PRCRCWGS*RPGTRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRQRPPRWITVA*SP R*PRCRCWGS*RPGTRGALPV VRKQPGDPKTPLASCPQLNQPV PEPAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSGLRLLGR PSHEGPWLKGTSCRS GTTCRDR PWV
28539	58907	A	28714	2	1580	
28540	58908	A	28715	286	352	
28541	58909	A	28716	1	531	
28542	58910	A	28717	1	1440	
28543	58911	A	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLQLVEVLPE ANRQLRQSGADGGQQA VF*F HRFLASVHQHKAASAPPYLFR IKCPVPLRAKPAALLIDNRLYG
28544	58912	A	28719	1	3534	
28545	58913	A	28720	1846	2121	
28546	58914	A	28721	176	462	TSRHSVYISDTCLKPRKSSKPTF CGCDLSFSPICHP/HGLSDVALI VQQLRQ*PLQPARLPVHWR HQNAVVDGVLSENGGAGWG RAWLRIRRS
28547	58915	A	28722	225	3465	
28548	58916	A	28723	937	1770	
28549	58917	A	28724	142	484	

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28550	58918	A	28725	1	1521	MIPITWPKFAELHPFCPEQAEG YQQMIAQLADWL VKLTGYDA VCMQPNSGAQGEYAGLLAIRH YHESRNEGHRDCLIPASAHGT NPASAHMAGMQVVVVACDKN GNIDLTLDRAKAEQAGDNLSI MVTYPSTHGVYEETIREVEVV HQFGGQVYLDGANMNAQRDD MAGKPGPLTVRKMGRGSRVTVR AL*/ASVWIGFDDHRRNLGHTT ASGAIKDQISGYEGGAKSAQPA WDAYMKAVLEGVPEQPLTPPP GIVTVNIDRSTGQLANGGNSRE EYFIEVNEIVNPNATLDWQLA LRQAAGKTDLARDMLQMLLDF LPEVRNKVEEQLVGENPEGLV DLIHLKHGSCGYSVPRMKNL CQLIEQQLRSGTKEEDLEPILLE LLEDMDNVAREASKILGGHDN GGNALLHKALPPGNVGVKAWAM APIPPPPFPQPGKSVTICWKPASS ENRSNLLIEFLRELISNASDAAD KLRFRLASNPDLYEGDGELRVR VDEVLSPASVPYS
28551	58919	A	28726	1	1279	
28552	58920	A	28727	3	762	
28553	58921	A	28728	1	1472	MTQDELKKA V GWAALQYVQP GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFIDLNEVDLSLGIYVDGADEIW QTCKAQRQCSPCKTLGAQPEN PDLSQLSRFPQDERRISNCSSGK AANPVLYWSKJEEKIASEPASIIY SPMTLKD FSKFVKDEIGFSYTG YSRSGGTASHGSPKSWAIGSL GRFGNEYSGWFDLQLKQRYVN ENGKRVDAVVMMDGNVGGQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFVVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWKVGP GKIDIALVR EDVDDYDRSLQNKQINTNTID LRYKDIPLWDKATLMPRIPTQR YGLAKA/SLEAD/VRY/MANAM GPEGVRVNAISAGQTRTLAAPG IK/DSRK/MLAHCEPVTPIRRTVT IEDVGNSSAFLCSDLSAGISGEV VHVDGGFSIAAMNERDPFTDL HRYRMNLNMMNYGAQRNM

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28554	58922	A	28729	2	419	RPRPRPHMLQGTTHQRHLHA GPGVARRRWGGMARRAAGRR PRLRLCIFSRSQLGLRLRFLSST VNEGQDVKTVA\RSGHFCGGLS SFSFSSSFSSGKKRPSNPGSMR LGSPSPGAGRAGGIVTVAC*AR LSTCNTKQ
28555	58923	A	28730	725	2804	
28556	58924	A	28731	661	1218	DVREGDRDPFMIVHSCVFVDF AKTMHDGA/SVSLRGNLISHKG EDRY/VFRDKSGEINVVIPAA/V FDGREVQPDQMINISGIADKLP VIAPTNATSKLKLASQPEDDSEI YDGCNGAQPGDYWFAAFVSG MFSRWLAKTILSRHILSVTIRSC KNGEWLAVGGAENGAYSDSR VAVMLLLSAWGLFDF
28557	58925	A	28732	1	624	
28558	58926	A	28733	1	1281	
28559	58927	A	28734	114	266	
28560	58928	A	28735	1487	1570	
28561	58929	A	28736	1	3402	
28562	58930	A	28737	1	2466	
28563	58931	A	28738	372	647	SGWSWNTKFPTGGFRWPAQPG TELESSQPR*LVMPATTSPFRAL DVCEYLPACVAVISGCHPSRFA RSYVSAPD*QNVQLTYPHIVLN RHL
28564	58932	A	28739	1	2235	
28565	58933	A	28740	3	293	
28566	58934	A	28741	737	963	
28567	58935	A	28742	3	282	RRLRASGCIDKLPSG**YARPAR *DPAPGFR*STPVRKCDQTRSPA MKVIAAADRKLCWGAICPLSA KPPAGRAPNAPAPASPNRPMPT PSL
28568	58936	A	28743	2	289	
28569	58937	A	28744	1	1662	
28570	58938	A	28745	421	2634	
28571	58939	A	28746	134	954	
28572	58940	A	28747	1036	1383	
28573	58941	A	28748	2	589	
28574	58942	A	28749	1	801	
28575	58943	B	28750	14	499	
28576	58944	A	28751	3	916	
28577	58945	A	28752	3	589	
28578	58946	A	28753	1	1675	
28579	58947	A	28754	1	522	

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28580	58948	A	28755	1229	1660	LMVSGFLTSPKDHRIIVAKPEQ FWKLKQVFMFAIVISLPTIGER FSPFLKLSPLIRPSRCGTTDFISG LTARPEFSQSRMVLIAASTITSL MCAGSFLPIRPLASICSLSNATTS **LPSSGRDSSRRKRRQTATCSP RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF NSIWSCASAILGNLIGITGSPPL ALCRTLCCLTYPI*CPRDAKALR RPRECVIRHD
28582	58950	A	28757	1	850	MPVMFLASLSGKHQGHFFPKG ERKFKIKERGTVATEDRRSGD STFYAIQPTRRQKRYYGLALLL QLHRRRQNLNIDSVSSVGLAAL VTAFIGVDFFFANGEQTYSQPLW TWMVSGDFNIGFNLVLDGLSLT MLSVVTEGYSR*EHRPTSPQPR YISSRLSASTRTTM/PGDEQVGV SEEARVALSDHREHGQRQAVQ HQVKTDVKVAYRHRPRPQRLAV CLLAVSEEINADKGGYQRRQA HRAV
28583	58951	A	28758	20	282	
28584	58952	A	28759	38	966	RDGLESRGVCSLRTAFQRSS EAFSTDQAELQNRASNRPAR IGHAHLVIFPVQSSWM*KLAS PRNNLVIPQEKALKEYIKGNLV MSLAAAPLNR*GLL/IEWNDND GGCKGACDRVPHQNVTAALNLR DQCINGECYDEVLFHGLEEYIN NLQGDGVIVLHTIGSHGPTYYN RYPPQFRKFTPTCDTNEIQTCTK EQLVNTYDNTLVYVDYIVDKAI NLKEHQDKFTTSLVYLSDHGE SLGENGIYHLGLPYAIAPDSQK QVPMLLWLSDEYQKRYQVDQ NCLQKQAQTKQKCVLLIFAKQ
28585	58953	A	28760	1120	1335	
28586	58954	A	28761	846	1245	TVRKRGTRHPHGSRRTLSPLR HSSDRCNRTSADRSTGPRL/A QPRYISSRLSASTRTTMPVTES MVSDRPSSTRLKPMKSPTDIH VHSGWLVCSPVAKKSTPMKA GTTAGRPTEPTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	A	28763	188	322	

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28589	58957	A	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE TTNRPRKVKIRHPVASFFHLFFR VSAIIVCLLCELLSSSFTICMSKK WLAIVVIVGVVLQGANLYGYLR CKGQEVRETFAEPSLQATQMK LKRARLADDLNEKIAQRPGPM ELVEKNILPVDSSVKEAIIIGKTL KIYYLGAPAEAAATKEDERTTSG PGHHATNYHFLKFDLYLSWL HFVHKDAILSGHPLVRLSTRV LRGPNDVFHGVSSVDSVLAIFV LAEPMGSLASLEN
28590	58958	A	28765	1	3219	
28591	58959	A	28766	3	245	
28592	58960	A	28767	2	1193	CANQLRDCLVIPITIGLVRLLV AGANGDRLGQPTVGADVRLSR CRKVMPSRSVEMGLVPSSSVIV TVLPLIGFVLLAFSRGRWSENV SAIVGVGSVGLAALVTAFIGVD FFANGEQTSQPLWTWMSVGD FNIGFNLVDGLSLTMLS VVTG VGFLLHMYASWYMRGEGYSR FFAYTNLFASMVVLVLADNLL LMYLGWEGVGLCSYLLIGFYY TDPKNGAAAMKAFVTVRVGD VFLAFALFILYNELGTLNFRM VELAPAHFADGNMMLMWATL MLLGGAVGKSAQLPLQTLWAD AMAGPTPVSAIHAATMVTAG VYLIARTHGLFLMTPEVLHLVG IVGAVTLLLAGFAAL*Q*K*HP RHPKHRNAG**TRVLQRGAGC AGAIRVTDHFRG
28593	58961	A	28768	3	2191	
28594	58962	B	28769	1	2263	
28595	58963	A	28770	1089	4965	
28596	58964	A	28771	41	249	
28597	58965	A	28772	533	709	VSFLIVSSSLIALWSEKQFVIVS LLHLLRSALLPTMWSILE*VWC GAENNVYSVDLG
28598	58966	A	28773	2714	3599	LGSQWH*IIYKLPWAVWFSQY
28599	58967	A	28774	45	188	GKVOCHRGLIHVNWLPPVKKF *LRQKGKPTSSSQETPKTEPGR LKP
28600	58968	A	28775	722	856	GNDLCPKTIRTGDAWCVPGTG RKSAWK*GKISGSLSFLPVRDG

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28601	58969	A	28776	474	1338	PANQKKPRTRWIHSRLPEVRR GAGTIPSETIPNNRKGNNP*LIL *GQHHPDTKTWQRJHNKK*KFQ ANIPDEH*CENPQ*NGKPNPÆ HSKKLIHHNQVGFISGMQGW NICKSINIHHNRTNDKNHMIISI DAEKAFDKIQHPFMLKALNKL GIDGTHLKIIAIFDKPTANIILN GQKLEAFLKTDTRQGCPLSPL LFNVVLEVLARAJRQEKEITGIQ IGKEEAPQKQRLFCRYHGGK RAPQLLITHLEEDDEWDIIRYY NVMSEEEIKRMKEIVKPKII
28602	58970	A	28777	2289	3225	LTNQNKSRTRWIHSRLPEVQR GAGTVSSETIPNNRKRWTTP*L L*GQHHPDTKTWHRHNKKRK QANIPDERQCKNPQ*NTSKPNP AAHQKAYP**PSQLHPWDARL VQHMQTNKHNP SHKQNVHDKN HMIISRDAEKSFNKIQQPFMLKT LNKLGISGTYLKIVKMHTMSSS HLFYLA LCLTFTSSATAGPETL CGAELVDALQFVCGDRGFYFM EQCTMAVSIRGRELLGPSEQEM LHKESGKQRQKANTIPVTSKIV HLALYATLLLFVMEQFLGESHK SREIFSFEQQISELGKESMKFSEE KEKE
28603	58971	A	28778	1177	1272	
28604	58972	A	28779	480	766	SSEIQHWFGQGPWRSCRVSGR RHEASTVLPLCFLLPQNSSSMQ LG*NRSM P/HVSESSRTLVL*EV TKHQVSSNFKMRDKDRSGRAS SLRKHRR
28605	58973	A	28780	1	1344	

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28606	58974	A	28781	971	2314	PTNQKKSRTRWIHSRLPEVQG GAGTIPSETIPINRKRNP.LIL* GQHHPDTKAWQRHNKKEEL* TNSPDEH*CKNPQ*NTGKPNPEH IKKLIHHDQVGFIPMGQWFNI HKSINVIQHINRTKDKNHMHSI DAEKAFDKIQPFMLKTLNKL GIDGTYLKIIIRAIYDKPTASILN GQKLEAFPLKTGTROGCSLSL LFNVVLEVLARAVRQEKEIEGI QLGKDEVKLSLFADNMIVYVE NPIISAQNLKLSNFSSKVSQYKI NVQKSQAFLYTNNRQTKSQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTFFTELEKTT KFIWNQKRARIAKTLSQKNKT GGIMLPDFKLYYKPTVTKTWK YWYQNRDIDQWNRIEPPEIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHH* GSIPSRSLLVATTPTRGVTAAL
28608	58976	A	28783	1	1938	
28609	58977	A	28784	1389	1499	
28610	58978	A	28785	1	351	
28611	58979	A	28786	1	329	KNLDEKLLPASSSSCRIWATSP VHHLWQVLKKILF/GLEPYEIST LFEQRQAM/LQSIKEGVVAVDD RGEVTLINDAAQELLYNHNFR SRSLPVFVLASACGSGTRRRRA
28612	58980	A	28787	1	419	VRPGHLLDIDDTDMPSLRYSDP EAQRIGQPFKGDDILKALNGEE NVAINRFLAQLRVFTPIYDE NHKQIGVVAIGLELSRVTTQQN DSRWSIWSVLFGLMGLVGLIGTCI LVKVLLG/IIFG*TYKSQLEFR QAMGRL

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28613	58981	A	28788	1	1795	MWII SCVMKRTAMNCVLWRK RRRKVCASIFGKNRANQKRD NVELFDARCPNLNDAADTVRY LPVLTVQLLDKQPRLTVLKKIL FGLPEYEISTLFEQRQAMLQSIK EGVVAVDDRGEVTLINDAAQE LLNYRKSQDDEKLSTLSHSWSQ VVDVSEVL RDGTTPRDEEITIK\ DRLLIITVPVRSNGVIIGAISTF RDKTEVRKLMQRLDGLVNYA DALRERSHEFMNKLHVILGLLH LKS YKQLEDYILKTANNYQEEI GSLLGKIKSPVIAAGFLISKINRA TDLGHTLILNSESQLPDSGTA CGQSLNVLYQRIVGERKLHTGS LMSAAGKSNPLAISGLVVTLTI WSYSWIFMKQVTSYIGAFDFTA LRCIFGALVLFIVLLRGRGMRP TPFKYTLAIALQTCGMVGLAQ WALVSGGAGKVAILS YTMPFW VVIFAALFLGERLRRGQYFAILI AAFGICTATQRNLLPCKNQPC KANQYQGTGDVNLQLHIDFRA FSGVMVAGSRQIFANEISSGAS NVGVVIFSTQDSANTFVNLNAS GGSRSVYPVMSDDMNGSSWK FSTRMQKIDPALSVTSQQLMSHV
28614	58982	A	28789	190	2058	
28615	58983	A	28790	199	293	RYPPAETELS*RLCRLLR*STTV RL*LCRPL
28616	58984	A	28791	685	1557	
28617	58985	A	28792	1	2850	
28618	58986	A	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR TATTQRHCRRMHMMTIGYQFQ PGALVR*SRANHFPGRGDVNLS SRYSNAPGRRRHQHMRRGFVA RSQ
28619	58987	A	28794	409	1305	

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28620	58988	A	28795	379	1703	LKTVLVDGVVKAELKVEGAKA VLRQAINGDLWDKAKRQPKLE PLKLSKIEATMSFTIAKGMVAQ TAGKHYPAPITAVKTIEAARF GREEALNLENKSFVPLAHTNEA RALVGIFLNDQYVKGAKAKLT KDVETPKQAAVLGAAGIMGGGI AYQSAWKGVVPMKDINDKSL TLGMTEAAKLLNKQLERGGID GLKLAGVISTIHPTLDYAGFDR VDIVVEAVVENPKVKYPSAG VFHQLYCRDVPVPMFAIYTFGP QIVGLLGLGVGKNAALGNVVIS LFFMLGCIIPMLWLNTAGRRL LIGSFAMMTLALALLGLIPDMG IWLVMFAFVYAFFSGGPGNG FNRVKEEFDHERFLVALTNYGT AMCAFEDAARYAN/LARAVWR GYWSFPVDSGKIRPHGDQIKLH EKHAV*SSVESRQRHHHLWRC SDVQILLRQCGI
28621	58989	A	28796	713	902	CRLARPSPKRCFCFSCSTTHSCI PPPLAATRWPVRRRWPRSPMCC WSRTYR\PG*AKRRYTSPA
28622	58990	B	28797	1	1521	
28623	58991	A	28798	348	599	RHFORSLSRSSDSNP*LDPTLFA SALASRQRVTESWSERHPDPLQ VRRKTEDVKTTPPFLQQSARHS VNIVLWIRGFSPDLLV
28624	58992	A	28799	582	732	
28625	58993	A	28800	1	1443	
28626	58994	A	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA SGG*TGETAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	A	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDH/K RPREALLDSLKKLQLDYIDLVL MHWVPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPTVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQG GKGVFQDKVIRDLADKYGKTP AQIVIRWHLDSGLVVPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDPDQFGG
28629	58997	A	28804	1040	1079	
28630	58998	A	28805	300	567	SAGFKKSGTRHCDVRPGACGT TLYQRR*VH*WSTVHKPETSS SKMHGQRGSLLAASLVANVI CSLIRNPLPIMPMLCAFVSLKM IKKRPRRH

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28631	58999	A	28806	167	327	KNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTDRRTN SPAYLSEL
28632	59000	A	28807	1	1197	
28633	59001	A	28808	1	4104	
28634	59002	A	28809	1	1368	
28635	59003	A	28810	82	1143	
28636	59004	A	28811	72	212	
28637	59005	A	28812	1	1078	MKDVTLVPRPDAGANTCAHIL SQLPHLQLPTLETGLINALGY APGDMQPSDSATWGVVLAELQHE GGDTFMGHQEILGTRPLPLRM PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQAVAGDNL EADLGQVYNITANLSVISFDDAI KIGRIVREQVQVGRVITFGGLLT DSQRILDAAESKEGRFIGINAPR SGAYDNGFQVVMHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ RVFAIFAVAIDITQVINIQCRC QQAACGRRKQCRNQSKENQY GNITQTDITRTIAHGVVIAAMI DNPPIRKPTKKS*LWWPLFY LLAVSLFTLVNRYRVFVHGLSAS SSPLRPTPY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVEDHNG YSGNACTRLHHAGGIRQ**PNF GYSPASSCGVVSQNSS
28639	59007	B	28814	1	2703	
28640	59008	A	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWTITTAVCV SSCRRWKKPAALVRPLPPASAP GFITTSAPKPCASRNG*KSSFQR TLHVSRRHQSRTS*SPOVDTSN SSEIVNNQAPTARTGSGRLVAV LEQRVQEPLAANAPQLRVSAI NAAS
28641	59009	B	28816	430	823	
28642	59010	A	28817	1	2667	
28643	59011	B	28818	204	2659	
28644	59012	A	28819	1	2817	
28645	59013	A	28820	1	1089	
28646	59014	A	28821	1	1891	
28647	59015	A	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRALPTEE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPYELPERRDPV SSAGALFVSRWIVERSCADKFR VFCGASGFR

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28648	59016	A	28823	1	1030	MMCMYRTASSLANQYHIDSE QARRGSQNAFDVNFEAWQLEI NHVLEAASQSQRNQYISALVF ISMIHVAIYISSALWWTRKMIV QPLAIIGSHFDSIAAGNLARPIA VYGRNEITAIFASLKTMMQALR GTVSDVRKGSQEMHIGIAEIVA GNNDLSSRTEQQAASLAQTAA SMEQLTATVGGQADNARQALG TGKNAATTAQAAAVQFIDRCQ ADFRGAYRYRSGTYFICQYLT VTVSGIDAHQRGQTDQTRILLQ LFLVQFDTHRQTLNDFDPVTGR ILRWKQLDRAAGDITGHRTDN TSTLQRQPGVTYFGGSLHGW *SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	
28650	59018	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLAFLWKKHFRFLDQVQN FYPSPLANSTMYTGNKPLAK IGYKSEDVFVPKGDQRRLLHK ALLRYHDPANWPLIRQALEAM GKKHLIGSRDCLVPAPTEEM REARRQNRNTRPALTKHTPMA TQRQTPATAKKAASQSRPVNA GAKKRPKAAELQCPLVMTSGN LSGKPPAISNEQALADLQGIAD GFLIHNRRDIVQRMDDSVVRESG EMLRRSRGFLPTGRGLRIDYKQ KMRGTRRAGCNFNQSGQGRPS LKRGIETDIKKAKKQATGLAG ESMLQDDAFYAVITHAAGPQG ALPLTPQMLMESPSATCSA*RR TPGWAGTPTSSPAKRC*LALRI TSSGSTPSCSRHRWRKRARRSD ACHHSRFSPTVWPVTPKQKGR
28652	59020	A	28827	1	1392	
28653	59021	A	28828	1050	1154	
28654	59022	A	28829	1	2649	
28655	59023	A	28830	59	511	
28656	59024	A	28831	1	2421	
28657	59025	A	28832	4594	4770	PSTSTIHA YVSGKSRISPHTR EAMNDHDKRAWLYALRRRAGR TRHRCPGRTGRQRL
28658	59026	A	28833	1	727	
28659	59027	A	28834	1	3069	
28660	59028	A	28835	1521	1841	FLPKSLGDSSGESRKHRRRRRA FSPDQHPAGNRYRTRLSARPFV* RCLYYSR*ARRGNRYRQH*TTSP ALYQAASPFQ*SIAG*RAKGR YRSSVYLCVDHFDHSGSW

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28661	59029	A	28836	1	1644	
28662	59030	A	28837	1	1245	
28663	59031	A	28838	1	1518	
28664	59032	A	28839	3	491	
28665	59033	A	28840	1092	2827	
28666	59034	A	28841	162	1760	
28667	59035	B	28842	1	3378	
28668	59036	A	28843	434	763	
28669	59037	A	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLENLPAADADQLAGN GGCHSQVRSIWIMGLHAFAC ETRMYPEEPVYLPPRYRGSIVH SIAF
28671	59039	A	28846	855	1134	PGNVLRLENLPAADADQLAGN GGCHSQVRSIWIMGLHAFAC ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCACNLCVAVWP VGCISLVS
28672	59040	A	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARHNAQQ EDALVEKAKQ/VTWRLAAGV CLLTVSS/VARADSLDEQRSRY AQ/KQAWDNQMDV/VFIHAM PTNTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCR ELSRRLRLHAQYQNTKRVHT QFSGYKTPMANTAVPTISSQR RALFNPH
28674	59042	A	28849	1	1247	
28675	59043	A	28850	533	1029	SKSIMLLCRSVVSMIRRTVAA FTLAAISVARSVLNLIIIDIGM QAMPLCRSTTGRNRWTSACK TILR*QRILPLTPC*HRMFRSL KKILSDGKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIQPAQ KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	A	28851	749	1050	SPHMPGITAGTPFSVPLAISPSI SAKSLPGKTA*AWPNIMALTPG ISLR**TEFSAILYGSADSPACA RTT/NIGTFLAHRHVFHAGFG NIIHRHFPF
28677	59045	A	28852	260	717	RQLRTELSAGIAAFRTGNAPAIL RFMKLAPP**WRRKPLTGV*RV *RGRDSVR*VAFVPTVSAIQQL DPRSLQQDAFKAGLDPEQPP KT/WQDLA/VLCRETSLRHEV RLRQRLAGLDPTGKL*AWNGM MPYDADAKDAPQKPLSAEPAC
28678	59046	A	28853	776	2730	

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28679	59047	A	28854	383	1367	RPTCWTSEIWWRRVRTAALRSS GKTWVFCCRRRIAGELMLTNR HTGGVMVTTFRASEAFAGALE LTGKATLVALINRCIGAVIRYM LIAVIPDIFQRLQVVLNVWILAV ANETTVRQRRVRRFKVDLVVR VHLLHIEVETVGVTTFIGHAR HHAKLSIETAEAIQVFTTRA VETETITRFFFLIHCLTQTFNN GDTFRAKLLVVNMLAAEQRV NGFVDADVTQRNRRTTVFEDF RNIIVSIETHATSTRYG*CVGPP AMRACSGAVQPQVWLHPGKL RQGEPSRDLVRQRPAAALCLPRR HRLRGYNGNIQRRLYSTGNGL
28680	59048	A	28855	1	1477	
28681	59049	A	28856	1	793	
28682	59050	A	28857	1	1020	
28683	59051	A	28858	1	613	SAGDGARIEQFDRKGMVNKPF NYFIMSKLAEGIPTQMERLLS DTECLVKKLDMPVECVVRNR AAGSLVKRLGIEEGIELNPPLF DLFLKNDAMHDPMVNE/SYCE TFGWVSKENLARMKELTYKAN DVLKLLFDDAGLILVDFKLEFG PVQGEVVLGDEF/SPDGSRLWA QETLEKMDKDGFRQSLGGLIG AYEAVARRLGYT
28684	59052	A	28859	1	1002	
28685	59053	A	28860	1	422	
28686	59054	A	28861	625	750	RNVQALQGAHGTGGALTDPAA* QHILGTLCADLL*NLSPSPRD
28687	59055	A	28862	1	1449	
28688	59056	A	28863	105	297	
28689	59057	A	28864	55	423	DRPQRNRATLMQLYSRSGPGIR RLEHRFEKVQKPGFEVFIPIGF KQKGLGRPLGVKALVFIDTGL FQLQAVKNLDGF*FDEASASQP GSDNILRELVRATGRADGSGT GFTEDANSFTSYR
28690	59058	A	28865	1	2340	
28691	59059	A	28866	314	696	

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28692	59060	A	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK CHGINPLRSWVG*VE*EEKY NMQT*E/LENWKPSNLHDMSS SHSKTLGYKRLTKSNPISCQILL YKSRSGRKNQRSTRTHCHHPS PKIYSASAKEPWILATNLPVEIR TPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDI MLLIALMLQLTCWLAGVHAQK QGWDKHFQANTVRNRNVLS VRLGMEVLRHSGYTITREDSLV AATLLTQNLFTHEEAPANSVPA AAVIRRVQALIGITGRKAHAGG SWNGTASSDNFPNIFILPQDNF MALAAAVAPPELEALLAAGKV SVKIQEPCEILFSRAKVWNGE KWACVTVIGGHTNIVHIETHDG VVFTQQAQVAEGEQESPLTVLS RTTLAEILKFVNEVPFAAIRFIL DSAKLNCALSQEGLSGKWGLH IGATLEKQCERGLLAKDLSSIV IRTS AASDARMGGATLPAMSNS GSGNQIGITELNVSCRFPATNL FVHDPTQQAMQRNQRRFAVQT FPVWRVAQIICAVRPFQRIGQ LRDIFHLKGDQFTNRPKAVAF
28693	59061	A	28868	2095	2722	
28694	59062	A	28869	789	2509	
28695	59063	A	28870	57	440	CSWDPQDPHGILQGAGKEDSQ AQKTTARQKRKTRKTATROKK HEKQSEESTNEDT*ARKVEETQ HKHDAESTSGSVIQGCQVLFQ SFTATPAASATTATRPITLCSSR ARAGVPSTTGVSRRRESPL
28696	59064	A	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK KGHFVVAHPA/P/DQFLHAAM DIKQPVISIDNLLAIHKQAEVTR FIGGDMQRA DRDHPRI AVALID KRIRFGISRRFRAQSIHIFRAQR MHIFRPVIGQHQA TGN SRLSAS TQRLHHPNPAFFGPFH
28697	59065	A	28872	1609	2112	HQPVLTVVMVPVPSLIIRADNP FRDEVGFLCPA VTVIPVKIVR VTGDTVIRPHAEGAVRVQLRV GQAVTCRVCGIRDADIQIRCGG VNAGQPAGGAVAVTPGLARAA DADEFV VVVPGVIAVRQQA VQ VLAL*LPGRGISGGEFITAEVRS VSRCRRSRVYSTRGIL
28698	59066	A	28873	2	712	
28699	59067	A	28874	337	383	

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28700	59068	A	28875	65	436	REVWEHAKRMLGDSLLDMGM DDELTVMVAYEYIGRLGKTATI HWKVKSSPSMVWSASVWKKM ALR*LSRTLRLPNQEHSL*ASVP ELKCAASWTKRKKNSTFIASSA IRLTL.TWKPKPFLSRL
28701	59069	A	28876	206	403	
28702	59070	B	28877	1	2046	
28703	59071	A	28878	1	1335	
28704	59072	A	28879	1	974	MEAPPIDVSSRDNRNRNRYGH PADLFWFYSLRALPEVYASSD AHEKFVKDFVAAWSLNLVYQR IVGERKLHTGSLMSAAGKSNPL AISGLVVLTLIWSYSWIFMKQV TSYIGAFDFTALRCIFGALVLF1 VLLLRGRGMRPTPFKYTLAIAL LQTCGMVGLAQWALVSGGAG KVAISYTMPFWVVFALFLG ERLRRGQYFALIAAFGLFLVLQ PWQLDFSSMKSAMLAISLGSV WGASAIYAKRLYARHPRVDLLA SLTSWQMHVCRQLASQLPLSH GAMPRCRRRPGHSSNPDRLANVI ARRVLRGMSNRQPVSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDNLNTQ LWISTNAFRFGN
28706	59074	A	28881	568	717	
28707	59075	A	28882	1760	3092	
28708	59076	A	28883	1	1206	
28709	59077	A	28884	1	575	MSGYSYSSVWAEDDIQFDSRFL LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKPQLAEEYDIWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPPSRWDDGIS GHADYSITAQTQHAKLNTEDD/ SNSTGSVWQGLWRLQDD
28710	59078	A	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YYAWRALPSLKAKLALGEDY LNSDIFDGFNYVGGSVSTDDQ MLPPNLRGYAPDISGVAHTAK VTVSQMGRVIYETQVPAGPFRI QDLGDSVSGTLHRIIEEQNGQV QEYDISTASMPYLTRPGQVRYK IMMGRPQEWGHHVEGGFFSGA EASWGIANGWSLYGGALGDEN YQSAALGVGRDLSTFEA

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28712	59080	A	28887	491	681	PTGHRAQKKWNT*TRHSNSY* KNFAKKLI*GDIREKLQKLEGF AGMNATQLIEVATEVYINCQDE AKKETEQLRKKANLLAAALT KRKINIVKGRECSHGCGHGRGQ VEQRAKRWLRGGRGWVKAFF VRTEKAREVTKVLLRDIIPGFG PLTLASDNGPAFIKIVQELTQL LKIKWKLHIAYWPQSSEKVEH MNQTLKQLLKFCQETHLRWD QVLPMVLLRVRYTPTKQTGY PMRSCSANLK
28713	59081	A	28888	1	963	
28714	59082	A	28889	123	593	KRQVLAGFLITPRRLPKNWT WCWWSM/PAQVKQVLFGETG VAQHLKPGTAVMVSSTIASAD AQEIATALAGFDLEMLDAPVSG GAVKAANGEMTVMASGSDIAF ERLAPVLEAVAGKVYRIGAEFG QVRP*KLFTSC*RAYILLPEPKR WHLPYR
28715	59083	A	28890	263	467	
28716	59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPLYT GLPRGPHGRAAGNPVDQQFAA GDLGLSPHADHPGGTDDVRW CLIST*KRWD SGV*AGAGQYSG WRRRSLRWR
28717	59085	B	28892	1	2118	
28718	59086	A	28893	1084	8334	
28719	59087	A	28894	2029	3313	
28720	59088	A	28895	1168	1236	
28721	59089	A	28896	1	284	
28722	59090	A	28897	1	1188	
28723	59091	C	28898	20	878	
28724	59092	A	28899	1904	2281	CSAYAGLHPFLWKSTRFCTHIL APATAISPNTTIDAPPITAAGMV *ISAPNFGKPNMAMTAAATN TSVE*TLVTAITPISA*VVTPLP PTEPESIVARPSPTNARPYGSIL RPVIPATALR

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28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV RLCWNLLISLGLWSCFSKGWVT TPITLSCSPPPRRGRMAPWAW GRSRARMCMWSWSWTRPSRPC AVRWSSSGATGSCWRRPVST APPRPPWPAPAAPTPAPLWART RMPSHWPSTTAPAAATAY*/DPD AGYQPTPLAAPAEPGSKYSLAS LDRGQGRGGGGGGALEYVPKA VSQPRRHSPVPSCKYVVDNSR PPTDLEYDPLSNYSARHLSRAS SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSPCLMWAASCRN PASLLASE*TVSNA*IPAERAAC KMEQRANSSSVPSGERSVRRLR T*SSAPRAIPKRSEA*AISTARVI PSGDSIAASRPVLPGRSPQAFSIR RISFSISRTS
28727	59095	A	28902	1	2916	
28728	59096	A	28903	1	2001	
28729	59097	A	28904	179	324	
28730	59098	A	28905	1591	1806	
28731	59099	A	28906	531	949	
28732	59100	A	28907	44	477	
28733	59101	A	28908	161	333	
28734	59102	A	28909	1	394	MEGVAFLTFLAARAAGVGNRPA SPQIVRKQREGHGILTRDPVA FDDVAVNFQTQEEWALLDISQR KLYKEVMLETFKNLTSVGKSW KDQNIIEYEQNPRNFRSLIEK KVNEIKDDSHCGETFTQVPDDR LNFQEKKASPEVKSCDSFVCAE VGIGNSSFNMSIRGDTGHKAYE YQEYGPYPYKQCPKNKKA FRYRPSIRTQERDHTGEKPYACKV CGKTFIFHSSIRRHMMNSHWEKP YECISKCDKAFHSSSSYH
28735	59103	B	28910	1	534	
28736	59104	A	28911	238	434	LPCKIHTPNHGPKLNIPSTKN*Q RRRNTSQR*LRHQPFSSASRPG SRLRFAIGLPAPAEAGMVT
28737	59105	A	28912	358	878	KLCHIAICHSVSFQCESFHVFTG FLSSVCPFMKSKIFDRSEGFPKL LTLIGVLSSVSPFMISKGSEGK GFPTLLTLIGFLSSVRFFMYLK* LGRIKAPPTYLTIFIRSLYRVHYV CLCPFMNSKVLGRSEGFPFTLT CIGLLSIVCRFPPTLLTLIGFLSSV SPYMISKGTGMR
28738	59106	A	28913	1382	1416	

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28739	59107	A	28914	1	333	MFQDPVAFDDVAVNFTQEWEA LLDISQRKLYKEVMLETFRNL SVGKSWKDKQNIYEYQNP FRSLIEKKVNEIKDDSHCGETFT QVPDDRNLNFQEKKASPEIKSCD SFVCGEVLGNSSFMNIRGDI GHKAYEYQYGPCKCQCPK KAFRYHPSFRTPQRDHTGEKPY ACKECGKTFISHSSIRHIVVMH SGDGPYKCKFCGKAFHCLSLYL IHERIHTGEKPYECKQCGKSFSY SATLRIHERHTHTEKPYECQCC GKAFHSPRCYRRHERIHTGEKA YQCKECGKAFTCPQYVRIHER HSRKKPYECTQCGKAL*YSLKS GSLMP*ALFFWLRIVLAMWAL LWFHMNFVVFNSVKKVIGS LMGMAWNLQITLGSMAIFMILI LPIHEHGMFFHLFVSSLISLSSGL
28740	59108	A	28915	1619	2353	
28741	59109	A	28916	1	1252	MSYSVMFALLLLTPLLFSLLCF ACRKRRLSATRTVTVLHSLGIT LLLILALWVVQTAADAGEIFAA GLWLHIDGLGGLFLAILGVIGFL TGIYSIGYMRHEVAHAGELSPVT LCDYYGFFHLFLTMLLVVTSN NLIVMWAAIEATTLSSAFLVGI YGGQRSSLEAAWKYIIHCTVGV FGLFGTVLVYANAASVCGTDH GGRMMRSWNGGQLISKLLAIT PDKLVLDGFSQAEDNIAVLKA QHISISAETQGAKEFTVDQLQ QSEYQLQPAFTVPPPTLWFVQR RRYFRISAPLHPPYFCQTKLAD NSTLRFRLYDLSLGGMGALLET AKPAELQEGMRFAQIEVNMGG WGVFHFDALQISISERKVIDGK NETIPTPRLSFRFLNVSPPTVERQ LQRIIFSLEREAREKADKVRD
28742	59110	A	28917	2	2282	
28743	59111	A	28918	518	1046	
28744	59112	A	28919	8	893	
28745	59113	B	28920	1	3129	
28746	59114	A	28921	1	1284	

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28747	59115	A	28922	3612	5412	PGLKHQNNHGRGPD AETKGV RDFGPN AKPLAG/VRLN/LERLR DTHHIDVAPLVARLDQMMEVS SQLQLARAGQSFSSGNYQHV KLLEDVILPSYDELSTMLDQRQ QTL L L PESAADITVQGDATLLR MLLRNLVENAHRYSPQGSNIMI KLQEDDGAVMAVEDEGPIDE SKCGELSKAFVRMDSRYGGIGL GLSIVSRITQLHHGQFFLQNRQE TSGTRA VVRLKKDQGA YPMSE KVVSQLSRK FIDENDATPAEA QQVVYYSLAIGHHLGVIDCLEA ALTCPWDEYLAWIATLEAGSE ARRKMEGVPKYGEIVIDINHVP MLANAFDKARAAQTSQQQEW STMLLSMLHDHJQENAIYLMG VFIMLIFFPAPVASEKPLSPDCW TTTTLRLMIGENSGLVSYMREK AVSPNCWNVIHYSGLFHLLELS SYDDVDN QIINTICEWISLIKTR GVRRPEFQTLTSGSGEGERFI MNRPTLFFTDLAHFVDRFTQYV HDTAQSRFTYRDFNRVFEVFI QTATQT VGGTHCDAPGW WFP GAVQSVPAALIAVAAAPGLA SFLPFARRVPRTVVALLAQAAA YADGMPARADGSFNSP
28748	59116	A	28923	1	2910	
28749	59117	A	28924	470	723	PGFGDARKLISLNFFIWV*TA* M*/P/LAGSDFVYRNS*RNVFIAQ TLQLRSRQPV TMHHATRAFQT EHNILRFECCEYSRYLFT
28750	59118	A	28925	599	1117	
28751	59119	A	28926	279	455	SLSHSSGRCSRGGISFVWVWF GPVACLAASVV*L*VSVVWLW LSPSGQGCLGCRVWL
28752	59120	A	28927	1	2913	
28753	59121	A	28928	1	2328	
28754	59122	B	28929	55	327	
28755	59123	A	28930	9	107	
28756	59124	A	28931	1	2106	
28757	59125	A	28932	1	1123	
28758	59126	A	28933	260	709	
28759	59127	A	28934	467	631	LEVIEAPQPNWS*SVQQSACST WPGCWVDLED PQV WVVYEW TTKRASLLPIFQD*LKALRKAQ VWAFAS*STWPGCWVDLED PQ VWVWYEWITKRASLLPIFQD
28760	59128	A	28935	989	3010	

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28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	A	28937	1	1006	
28763	59131	A	28938	185	384	
28764	59132	A	28939	2	615	WAFRVIRFIVTANWSLKAVWM RRLIVVA/ALLTLRTVPMRQLNR LLLITPSLSRHMVSTGPAATSCVN RGFLSPTVVSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGE QISLGVRNTSPDVPYLIQSWVM TPDNKKSADFIITPPFVFLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRAVPSTTKRKEGNTLKIAHK RMITN
28765	59133	A	28940	1	1686	
28766	59134	A	28941	76	981	
28767	59135	A	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPHRQWSASYWRS *SSSFRNLNKKCHTQNHNSCIKM ARE

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28769	59137	A	28944	1	2539	MPIEELALRSWQRPFLK WAGG KYSLLELDRLIPAGKRLIEPFV GGGSVFLNSDKHERFLADVSA DLINLYQMLAVVPDSVIYEAM KAFRHLNDAENVTILIREAFNAQ RLDAVERAAAFYLYLNHCFNG LIRYNLDVFFNVGFGKHQMT NNEKSGPFEGLLVIDMTHVLNG PFGTQLLCNMGARVIKVEPPGH GDDTRTFGPYVDGQSLYYSFN HGKESVVLDLKNHDHKSFGHT GPLKDA PAYDTIQAMS GIMME TGYPDAPPVRVGTSLADLCGG VYLFSGIVSALYGREKSQRGAH VDIAMFDATLSLEHGLMAYIA TGKSPQRLGNRHPYMAPFDVF NTQDKPITICCGNDKLSALCQ ALELTEL VNDPRFSSNLRVQN QAILKQYIERTLKTAAEVWFT PFSNKYNGHRIARTDKASMPVT YSESLFVEGIIRASTSMITKQGP SLRTGRTLRKFCPLSETAATDTS SIFPSKFTPTASRLPGFSIRSPK MTQSVLLPPGPFTRRQAQFTT TYSNITLEDQGSFHLVVRDT EGRMASVQTRPPADREAFTRI LPEHTLYPHTPAIAAGVFIDGDI PMTTTQTHDLAPANQPEFELTV TPVPDEQRIDFWPQYFGAIPQW LLEPHIFAWMDRFCEGYSGGI WSFYTLNNGGAFMSPEPDNDET WRLFNCLNATMPPYRMTCGTV
28770	59138	A	28945	907	1917	
28771	59139	A	28946	1	3033	MVWGFTCSSTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQIDTLTQMMTSTLFSPPSV HNVMETVTQETAPPEDEMTTSFP SSVTNTLMMTSKTIITMTTSDS TLGNTEETSTAGTESSTPVTSAV SITAGQEGQSRRTTSWRTSIQDTS ASSQNHWTSTQTTRTSQTSTL THRITTSPTSPSPSVHNVGTIVSQ KTSPPGETATSSLCVNTNTSMM TSEKITVTTSTGSLGNPGETSS VPVGTSLMP
28772	59140	A	28947	636	725	
28773	59141	A	28948	1	1123	
28774	59142	A	28949	2345	3644	

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28775	59143	A	28950	34	437	CGRLLQKSGFVVSVGIDGIERL NTRRARGLPNGTACGQQFSSFR GAFCTQVAHIVFCTEGD TDQ/D ARKRERFPLRG*SPA EIQSP PAG RCCRVHDHRLFRYAGSFFQYPE HPERYRFSADAQRP HHRERRLP
28776	59144	A	28951	1	457	
28777	59145	A	28952	176	757	KPMKSTAAAADAALLSAERQ VIDDAAAHLSVAQGGDDVD AI EQAIKNVDKQTQDFAARRMDQ SVRRADRSDLIETFDHVCTVIFI RDGITS AEVETADTARGNV DVI RTGEVGAVCGTEETKSILQYLQ YAIKDFATLCVLLQDGKNNV LLTHTSQVFQPHIFAESDQLRN RRIFGDRFDSVPSIRMMFGI
28778	59146	A	28953	1	1503	
28779	59147	A	28954	425	619	AGWSFLPSPA EQNRWRFP LSRF CQIPAPLQVRS* LACRFFAA YSP PLLKSPAASMA YTTSR LH
28780	59148	A	28955	55	476	SYHALANVFYQRRMAITQVAG RQAVQFKAHLRDDVHHHIDGQ VTATESVMEGNRHAVL*TRAT NRFFQVGAQFAIARFFSLVGLL WRVLES GKIASFATIPGRYPFLS LRLFNLRHFDCLILRGCRKVL HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	B	28957	12	271	
28783	59151	A	28958	309	1238	GS GSCYSALVKRKWSARSLRA DRNGARRGAYVGRKFHFGPG LAGFFSAHASNLRRSDRAPAH YHQLLNFPADPVDMMQ*KRGM VFLLLM DQQRQVDDWRRLPS LLSVWQSCGDSGRRAPGGR*FH WRFQATVFQALAE DLRRNLQ! VVATVAF/GMGINKPNVRFV VH FD/PRNIESYYQETGRAGR/DGL PAEAMLFYDPADMA/WLRRCL EEKPQGLQD/IERHKLNAMGA FAEAQT/CRRLVLLNYFGEGRQ EP/CGNCDICLDPPKQYDG/STD AQIALSTIGRVNQR/FGMGYV V EVIRVA AFLEPDYSHRP
28784	59152	B	28959	1	2123	
28785	59153	A	28960	1	2834	
28786	59154	A	28961	1	2505	
28787	59155	B	28962	145	494	

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28788	59156	A	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHAF*PLLGDFGCRNGVVIQGRENAHLMNGGGRRVTALHFQQYRFHHLFNILTARHHLIDNANHQAQIDR*RFAMRLAGGTATHQ
28789	59157	A	28964	1	1423	
28790	59158	A	28965	1	863	
28791	59159	A	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	A	28968	1	1215	
28794	59162	A	28969	1	1678	
28795	59163	A	28970	1	4674	
28796	59164	A	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFQHQLIAGDHFHHFQAHLVQFGGDFQLFNLGEGQLVVSIFTPVRLAVHGVKIE TVFVGFSSLIHGSQTVLVSSASG ASVASTRGKCTIVTSGISG/VIA KND/GLPRVHGATAPSCASQFL VFAAPTRPRDRHG*RTDDSTPQ RLSSPAVEKAPTASSAGNSRN DKPLREITLITSDRPVPDAAVSP TGFWPLTIPFHCRRMSSLPGIPI RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSGRRAPGGR*FWH RFGHGHGFPAGGGSPAKPVNR RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	
28800	59168	A	28975	904	1473	
28801	59169	A	28976	738	893	
28802	59170	A	28977	1	1108	MADTRYFGMHMSQETPASTTE AQIKNERRISPFWLLPFIALMIA SWLIWDSYQDRGNTVTIDFMS ADGIVPGRTPVRYQGVEGTV QDISLSDDLRKIEVKVSIKSDMK DALREETFQFWLVTPKASLAGV SGLDALVGGNYIGMMPGKGKE QDHFVALDTQPKYRLDNGDLM IHLQAPDLGSLNSGSLVYFRKIP VGKVVYDYAINPNKQGVVIDVLI ERRFTDLVKKGSRFWNVSGVD ANVSISGAKVKIESLAA
28803	59171	A	28978	1	861	
28804	59172	A	28979	5	337	
28805	59173	A	28980	1	612	
28806	59174	A	28981	128	1742	
28807	59175	A	28982	1	2688	

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28808	59176	A	28983	361	738	FLQPPFPFKREINKFIRDIANNMK TDFSAVTLFTDCVTVMLWII*F FQRKFLLKGF*PPLGSFYRE*IT SLFLYLLCNIFLATHRISCDDFSF NIQHVKKFWDSNLIIRFLRLDL SDDQTVHC
28809	59177	B	28984	1	1263	
28810	59178	A	28985	363	569	KGYRRSGKHRQGCCNVLRRL FPDQHTAPRPMPLKRQTRAPGQ SPPLGADPHPGQF*LPLLRGRF AR
28811	59179	A	28986	1	1035	
28812	59180	A	28987	275	721	LMVSGFLTSPKDERIMSGEAR AILIASNSSVLCAFRNFKSFT DLLPSELAQSASERISFNNTLKD SGMPGSI*WLPSTMFLYLVRPF TSSDLTVSISCRVYAAPYASSA HTSISPKR*PPNTQRLLTGPGVT FWGRKPPLFPTP
28813	59181	B	28988	1	2082	
28814	59182	A	28989	1	1567	
28815	59183	A	28990	1	453	
28816	59184	A	28991	1	777	
28817	59185	A	28992	1	1431	
28818	59186	A	28993	1	561	VDSRGYPYSGRGAGKCRESERL GSESRNPGSIGLENELTAEDVAS ADMVILTKDIGKFEERFAGKTI VRVNISDAEFLMTNRISRLKTA LFANTREISLERALLYTASHRQT EGEPVILRRAKATAYILEHVEISI RDEELIAGNRTV/ITARRDYVA GNGPLLAERAGSIPDASAGPL CYQRRRL
28819	59187	B	28994	1	3414	
28820	59188	A	28995	1082	1297	MIMWLAAVAIREINHDSGSATF RTPRPRTVAGKYNLGASLYK SELLA*LHSAGAGCLSCQRAKL GLGRKR
28821	59189	A	28996	1	2115	
28822	59190	A	28997	168	317	
28823	59191	A	28998	1331	1471	RWSNGTLENGTL*LLTLPSASLI STNKSPLDDVE*RSLSKAPGDT
28824	59192	A	28999	147	1456	
28825	59193	A	29000	1	439	

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28826	59194	A	29001	722	2805	TPRAERTASSVALPTSRLLRAR AETTTAPSTPMKTHRVISMVFF TCSQTGTPSASPVKSSLKVSSLN IIIASTTNRPS/VQQF/WPVSPPG DGTRRYPISISLTVLTGNDNVNL LRAGIDLAIYFDDAPSAQLTHH FLMDEEILPVCSPEYAAQRHALT DTVINLCHCTLLHDRQAWSND SGTDEWHSWAQHYAVNLPTSS GIGFDRSDLAVIAAMNHIGVAM GRKRLVQKRLASGVYPPRCAY PRTHLETTSTSGVNGVGTYS PFWRMLLNSFVMAFSITLGKIT VMSLSAFAIVWFRFPLRNLFFW MIFITLMLPVEVRJFPTVEVIAN LQMLDSYAGLTLPLMASATAT FLFRQFFMTLPDELVEAARIDG ASPMRFFCDIVFPLSKTNLAALF VITFIYGWNQYLWPLLITDIDL GTTVAGIKGMIA TEGGTTEWNS VMVAMLLTLPPVVIVLVMQR AFVRGLVDNPAANYIHVGVR SGMTAIAAGIAHHGGFVPTAT FLMFVEYARNAARMAALMKA RQIMVYTHDSIGLGEDGPTHQA VEQLASRLTPNFSTWRPCDQV EAAVGWKLAVERNHGPTALIL SRQNLAQVERTPDQVKEIARGG YVLKDSGGKPDIIIIATGSEMEI TLQAAEKLAGEGRNVRVVS STDIFDAQDEEYRESVLP ARVAEAGIADYWKYVVG
28827	59195	A	29002	2253	2546	
28828	59196	A	29003	279	629	NGAGHL*RPVVDGATAAPAGG RYAHLRVCPESLPWLHLP YRSGS*SAPCHCRNHRSGSAWQ KHYGNRFRFRTVVRPYRGRALH LRGRNTAITQAADWRLATAQL LEIAGVGDE
28829	59197	A	29004	313	638	RWRQRWFVWCLHCLVLFRTPR TFALSQCPRWDSDRSQDTSM SIQWNRMYCNCMSQDEQE ANGKGPAQVQDRQAWAGR/CR SHRREGTIPGNPHPRAS* RAGWQR
28830	59198	A	29005	1	1182	

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28831	59199	A	29006	1	535	RPVVLPIVAGSNALGAILGYVES ALEIAQQCEGAVNISSVVVASG SAGTHAGLAVGLEHLMPESELI GVTVSRSVADQLPKVVNLQQA IAKELELTASAEILLWDDYFAP GYGVPNDEGMEA VKLLARLEG ILLDPVYT GKAMAGLIDGISQK RFKDEGPILFIHTGGAPALFAYH PHV
28832	59200	A	29007	1	1953	
28833	59201	A	29008	1	656	MKLMAIQEQARGEQCFRDSEW DLQFHIQVALATQNSALAAIVE KMWTQRSHNPYWKLLHEHIDS RTVDNWCDDHDQILKALIRKD PHAAKLAMWQHLENTKIMLFN ETSDDFEFNADRYLFAENPVAI AKELELTASAEILLWDDYFAPG YGVPNDEGMEA VKLLPRLEGIL LDPVYT GKAMRGLIDGISQKRF KDEGPILFIHTGGAPALFAYHP HV
28834	59202	A	29009	1172	1371	
28835	59203	A	29010	338	528	RHPRCDPYGFCPFTADADDA** LGACHHYWRGQRKIYAGSGDS RCQPDGRRSAPARRPLRRQR
28836	59204	A	29011	413	2798	
28837	59205	A	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P SSFKEGIDHSATFFFAARFALVA AAIFCVFADGFFAFLASFFAAG FVFFSPRKALSGSKFTFLPT

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28838	59206	A	29013	767	1428	FTPLSLRAVVIQLANRQYLDEK SDRAVHQGHIPRQFY*SLRRNL TNRHQLIAIGGAIGTGLFMGSG KTISLAGPSIIFVYMIIGFMLFFV MRAMGELLNLEYSFSDSFAS DLLGPWAGYFTGWYWF CWV VTGMADVVAITAYAQFWF PDL SDWVASLAVIVLLTLNLATVK NVGEMEFWFAMIKIVRPLSGSR TKKMSKSDNNRNVIGLLED KSVVKKIKRAVTDSEPPVVRV DVQRPKRSALLERAPERFQEVF ILKGREDKRLPLIHAIHESQGG GYPVGKPPISREKRPCRASGA YSPVLLILIMDPLGNLPFMSV LKHTEPKRRRAIMVRELLIAL VMLVFLFAGEKILAFSLRAET VSISGGIILFLIAIKMIFPSAGNS SGLPAGEEPFIVPLAIPVAGPTI LATMLLSHQYPNQMGHLVIA LLLAWGGTFVILLQSSLFLRL GEKRVNALERLMLGLVMMAP
28839	59207	A	29014	1	632	
28840	59208	A	29015	1	1215	
28841	59209	A	29016	38	457	LNRLKLVAHSQSSRAMVFSSI RSFMFFSTLFLVRRQFSR*TIML SANSDSLTSLLPIWLLFISFCLT ALARTSSTVLKRSGESGHPCLV PVFRGNTFNFSFIMLAVGGV LHCEINCRICSTGRSANPLDSCI
28842	59210	A	29017	899	991	
28843	59211	A	29018	1740	1868	
28844	59212	A	29019	1	1084	MSAEITAPWYRLQLDLFTKLVA TCMEQFRPKTIPLAIPERLNAH CEELYELIASNNILNLYMPAG QEAHRFAMGELPDEVLEICQR LAKLTEMLRGLAELFLNDLSEK TGSHDIVRLHRLIQMNRLGM FEAQSKLWRLASLAQSSGAPVT KWATREEREGQLHLWFHCVGI RVSDQLERLLWRSIPHIIVTSAT LRSLNSFSRLQEMSGLKEKAGD RFVALDSPFNHCQGGKIVPRM RVEPSIDNEEQHIAEMAFFRK QVESKKHLGMLVLFASGRAMQ RFLDYVTDRLMLLVQGDQPR YRLVELPANASPTVSAACWW AYSHLPKGLI*KVICARCISTK SLFRPSTARW
28845	59213	A	29020	1	2022	

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28846	59214	A	29021	878	1267	LNSWLPSPVPTV*SSVFNAL*TG* ISPAFNPFADM*SASGLP*IKSPL STSTLFFTSRLASLRLA VRTSPN FSVAVSL**SKSIMLLCRSVVSM IRRSTVAAFTLAAISVARSVALN RFLIKSTGNACK
28847	59215	A	29022	294	2305	
28848	59216	A	29023	5	337	GAPQHQMMSYRINGRESPML TYPSTPNFFWLA WQARDFMSK KYGRRFPARFLWRSTPAGVVR KTIFIFISLVFVLMCANSWITI RTSAAAGCHCQVVCAGMNTW RVG
28849	59217	A	29024	1	1753	MPSTRYQKINAHHYRHIWVVG DIHGEYQLLQSRHLQLSFFPKID LLISVGDNIDRGPESLDVLRLN QPWFTSVKGNHEAMALEAFET GDGNMWLASGVYRIPLA VIWII GSLTSKAYKAEVQQRREAFNR AKMDYDHLVRQIQVGGLEGF IAKRTMLEKMKDEILGLPEEEK RALAALHDTARERQKQKFLG FFIDVASIPGVGPARKAALRSFG IETAADVTRRGVKQVKGFGDH LTQAVIDWKASCERRFVFRPNE AITPADRQAVMAKMTAKRHRL ESALTVGATELQRFRLHAPART MPLMEPLQPTSVVVDKVVKEK GTKEVAEAYLKLYLSPGQEI AKNYRPRDAEVAKKYENAF KLKLTIDEFFGGWTKAQKEHF ANGVIAVVAAGIGYWKLTGEE SDTLRKIVLEELTNQQQNQNP SPCAEVKPNAGYVVLKDLGSL PYLLMPTYRINGTESPLTDPST PNFFWLA WQARDFMSKKYGR RFPIARFLWRSTPAGVVRKTIF ISLVFVLMCANSWITWRTSAA AGCHCQPTGIAQALLSTRQHGG AQCPDLLPLSPLSSSF
28850	59218	A	29025	865	974	IMPRISGSQSGEHQQPLVATAR WFARA*ILIIL
28851	59219	A	29026	1936	2490	
28852	59220	A	29027	1105	1518	
28853	59221	A	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	A	29030	3338	3553	
28856	59224	A	29031	95	1289	
28857	59225	A	29032	1	732	
28858	59226	A	29033	1	672	

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28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTTTL AEGGLEAAEEAGIPLVNVHVG MFGIFTDAESVTCYQDVMAC D/GGTL*AFLPYDAGRRLQHG RYQ
28860	59228	A	29035	852	933	PAPYALLLLPMHPHGLRRDR QGRHNLNDRRRHWHVRVCH LLRRERSRKDAPADGHPPLRA VGGRNQN*FGE LR TTTCTQT D FLT FNLT SVTSNEASFTQFR TQG LVVFHQSGAGDTVDR TSL TRDT TTFNGDVQVQFLNHVDQFRL TNYHAGSF TTEVLFQRTLV DYD FTVARFDENASCGTFAATS AVV LIFSHCLRLLCRVVVLVTR VNF QFTEHSTTQRAFWQHAFNR DF NHTLRTASNHLFKGRLFD TDDV AGVVIVHFVSTLVAGYSN FVSV QNDDVITGIYVRSVFRFV LTAQ ATSQFSSQTAQSFTGRV NNIPV AFYGFWFSCAKYYRHGA RWCS NGRKIDQRHTHCFCCPC IRTDFA VEIGKEEFIT
28861	59229	A	29036	1	797	MIVFIENFKTSSPKYADILL PDL MTVEQEDIJPN DYAGNMG YLIF LQPV TSEKFERKPIY WIL SEVAK RLGPDVYQKFTEGRTQE QWLQ HLYAKMLAKDPALPSY DELKK MGIYKRKDPNGHFVAYK AFRD DPEANPLKTPSGKIEIY SSRLAEI ARTWELEKDEVISPLPV YASTF EGWNSPERRTFPLQLFG FHYKS RTHSTYGNIDLLKAA CRQEVWI NPIDAQKRGIANGDMVR VFNH RGEVRILPAKVTPHPV GTWTA E
28862	59230	A	29037	1	1019	
28863	59231	B	29038	1	2727	
28864	59232	A	29039	1	2250	
28865	59233	A	29040	1	2850	

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28866	59234	A	29041	1	1339	MTGKCGKFGNFLESWRAQKGTG ICGKVWNFLENLLNGFGQNAY SDTDNEVQAEVVSDDKDELVG NWSKGHSCYAKRLAAFCPLR DLWNFELERDDLGYLVVEISKQ QTIQEEADHKNLESQTEDAIE KKTPFSGEKFLAAEICISNKDP NINSQDDGENVPRVAVHPNGC FAWKLPVLSRKFERKPIYWILS EVAKRLGPDVYQKFTEGRTQE QWLQHL YAKMLAKDPALPSY DELKKMGIFYKRKDPNGHFVAY KAFRDDPEANPLKTPSGKIEIYS SRLAEIARTWELEKDEVISPLPV YASTFEGWNSPERRTFPLQLFG FHDKSRTSTYGNIDLLKAACR QEVWINPIDAQKRGIANGMMP YVFSSQMAKFTPRTLGLSLIWK AHKCGEAETLQKQ*C*QSGAT LPAGPRARAWPPYPRLPFTGLA CVDLHGNARKAT
28867	59235	A	29042	378	530	AFLPYDAGRRCPLPGTVSV*SGL YVRGAQHGRYQ*HHRCTSDK IWRADKG
28868	59236	B	29043	1	1617	
28869	59237	A	29044	417	607	
28870	59238	A	29045	954	1163	
28871	59239	A	29046	444	3793	
28872	59240	A	29047	475	732	
28873	59241	A	29048	1	219	
28874	59242	A	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	A	29051	1	411	
28877	59245	A	29052	172	378	LSLLRELGPVVAALLFAGRAGS ALT/VRNRPDARYRATLQYGD DGGGSAASGYFSPFLGWGYFIT TVDG
28878	59246	B	29053	1	1641	
28879	59247	A	29054	1	3036	
28880	59248	A	29055	1	1419	
28881	59249	A	29056	1	1500	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
28882	59250	A	29057	2	1760	KSQQLHDPPCAPIQQEAVRAVV GQPPQQHLGFPVERGVQCQREC DFEKELEARIASLSDSVSNAREE RMALRQEQEQI.QSRIQSLMQR APVWLAQAQNSLNQLSEQCGEE FTSSQRTHHGSEGNITKRGLLG ELRFENGDPSPNDQSYGRHKDG MAEIGTFHGGDLRGLTNKLDY LQQLGVNALWISAPFEQIHGW VGGGTGKDFPHYAYHGYTQ DWTNLDANMGNADLRLTLD SAHQRGIRILFDVVMNHTGYAT LADMQEYQFGALYLSGDEVKK SLGERWSDWKPAAGQTWHSFN DYINFSDKTGWKWWGKNWI RTDIGDYDNPGFDDLTMSLAFL PDIKTESTTASGLPVFYKNKMD THAKAIDGYTPRDYLTWHLNQ WVRDYGID/GFRVDTPKCLRCN PSITIGTNYAS*PQWSSIPGAL* G*/PAWAG/GLPWAPSVLLLDH LRQGTMTLEENLGNITQDIGMG KDFMSKTPKATVTKAKIEKW LIKLSFCTAKETTIRVNRQPT WEKIFAIYSSDKGLISRIYKEL QIYKEKNKQPHQQVGEHEQT LLKRRHGCSQQTHEKMLNHQ
28883	59251	A	29058	1	1119	
28884	59252	A	29059	3	2599	
28885	59253	A	29060	225	1245	RGSTGAHPRSAGKHYAKTSA NAAGDP*YQMGPHHRGCGKP VLPDPHQSENLRWW**RAWCG SGGYR/MAEGRHAAQGIIDWLG LDVDKLGALFERRKVLQVTE NLQAERNRSKSGQAKARGED IEPLRLVKNLGEELDAAKAE DALQAEIRDIALTIPNLPADEV VGKDENDNVEVSRWGTPREFD FEVRDHVTLGEMHSGLDFAAA VKLTGSRFVVMKGLIARMHRA LSQFMLDLHTEQHGYSENYVP YLVNQDTLYGVGLYPLGALAS GWLPRRERKDATPGTGYPG AHGNLELPERSEGPRAGGEP RTGHTQKGSPPDRGQTPPKGP
28886	59254	C	29061	201	1244	
28887	59255	A	29062	1	2530	
28888	59256	A	29063	675	920	RTYRLAGRKQRRGGGTDSSRS QNPWRSHRRHL*RSSGAGKR GGKRFAGGAERNRPLCRCKPEP PAGGDRRRRLAAAGAD

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28889	59257	A	29064	498	707	
28890	59258	A	29065	510	554	
28891	59259	A	29066	600	734	PECLSPADH*YKHCSTGTQAR QPDADCP LLPRLAAHNERQTR
28892	59260	A	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD LWPGEV LGIVGESGSGKTLTLK SISARLT PQQGEIHYENRSLYA MSEADRRLLRTEWGVVHQHP LDGLRRQVSAGGNIGERLMA GARHYGDIRATAQKWLEVEIP ANRIDDLP TTFSGGMQQLQIA RNLVTHPKLVFMDEPTGGLDV SVQARLLDLRLGLVVELNLAV VIVTSSPDQDWGFTPEPRLAAR FPGSTHSSRRNRGRHRPRRS LPTPSAPHSRAPGDGVKL VPPP ARVTRNEPAPSDSVTLGV PHEP GACIGTPILTFVRPSTSAINAAA EESTGTILFGAGGFKRTLNDT ESDSTTLVASRYWDLSSGWQR AINLRWLDHFTQGEITNTTML FYPGVMISRTSRGGLMPTWG DSQRYSIDYSNTAWGSDVDFSV FQAQNVWIRTL YDRHRFVTRG TLGWETGDFDKVPPDL *LKSR VGQRSELGSGYTTPRARVEPPKL LSRKVRAHFGSRAPAGRA*RH LRAPDCGVRVWVWAGSGAGDG GGRGCGSGTSEWILGSGRRGE
28893	59261	A	29068	84	128	
28894	59262	A	29069	1547	1822	CSRCSIFAFRVKPAPLKPRVFSP AWNVPRL WHLAPSTFSGGEQ QRVNIAR/ELYRRLPHSAA *RN YRLP*QNQAALSRLYA AFLPR POYHH
28895	59263	A	29070	1520	1656	
28896	59264	A	29071	563	976	
28897	59265	A	29072	1	1011	
28898	59266	A	29073	1	1097	
28899	59267	A	29074	1	2490	
28900	59268	A	29075	1	879	
28901	59269	A	29076	1	1317	
28902	59270	A	29077	1428	1619	YAAARRALCGSPCFPGGCNGE NCRLPPQLHADLTARIFYETRG WWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG* HQLWARWQNGLAHTPRADS THQQSALDGRISLIT

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28904	59272	A	29079	1886	2329	PLL V W I N T R P S L T T G R E S A S P A T L V C H A T V P S L V I A S H V L S F L * W S F T V L V I S R I G V A F A H A I F W S I T A S L A I R M A P A G K R A Q A L S L I A T G T A L A M V L G L P L G R I V G Q Y F G W R M T F F A I G I G A L I T L L C L I K L L P L L R R T V K Y T S G C
28905	59273	A	29080	1	2319	
28906	59274	A	29081	3	194	STSSLA A Q S L R F G Y E T S Q T G L A T Y C G E K I Q * F F A D L Q P V C A D S Y P L L V Q M K K L G P I V F F F D I
28907	59275	A	29082	3109	3384	
28908	59276	A	29083	703	1000	D C F L R R L I K R P F G T S M K D Q A V R F E E G F M A M G A L G L A M V G M T A L A P V L A H V L G P V I I P V Y E M L G A N P S M F A G T L L A W I W A A V F L A K E L A G G V R L L V L I F
28909	59277	A	29084	2040	4603	
28910	59278	A	29085	3	94	
28911	59279	A	29086	3	148	Y A E H M L E V M S S I G D Y T / N P R P A S R P V T K F D Q R G H R L G H G V W N L M F E R V K
28912	59280	A	29087	27	227	
28913	59281	A	29088	344	1067	
28914	59282	A	29089	798	1049	
28915	59283	A	29090	1	1473	
28916	59284	A	29091	1	720	
28917	59285	A	29092	45	208	
28918	59286	A	29093	1	2499	

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28919	59287	A	29094	1	725	MHPRFQTAFQAQLADNLQSALE PILADKYFPALLTGEQVSSLKSA TGLDEDALAFALLPLAAACART PLSNFNVGAIARGASRRSAKNIP RAVRQVFWRILLFYVFAIILSLI IPYTDPSLLRNDVKDISVSPFTL VFQHAGLLSAAVMNAVILTA VLSAGNSGMYASTRMLYTLAC DGKAPRIFAKLSRGGVPRNALY ATTVIAGLCFLTSMFGNQTVYL WLLNTSGMTGFIAWLGIAISHY RFRRGYVLQGHNDNDLPYRSGF FPLGPFAFILCLIIITLGQNYEAF LKDTIDWGGVAGTYIASGGPEPA VNSHAFGVLRNVVSIIVFFHQF GDAIKRLFPTDLLPFIRTWRTVF RKLQTAFGVDEIHQASAFRTKC TAVDRVIRIAFDMDRLDFFSWR SGYISRIPLIGLYFACALERHQN ERQPIILSDQNAIATINQLAIER DVLNCRVRIARSLSELVAIREEIE PLLIINNSHYLLDDAVNNYITVK NIITAAGIEQIKHFLATAFIROQP ERFFSAPGSFHYSNVRGESWQH ITRQICACLVAQHHTADEAQRI IAREGEGENLIVNRLAIPHCVSE QERRFR*TVAWWRAA*CAVCD DGDRCRSVLPDLHVWQPDGIPV AAEHLRDDGIFYRLAGDCH
28920	59288	A	29095	3	453	
28921	59289	B	29096	1	3684	
28922	59290	A	29097	1	231	LLVFINQEEADFHTQRGGPVFQ QATFTL*QLALFAIEPGLMTDP DIQVRGTTLPYGRGAAHGVT SNWKLTFRRILY
28923	59291	A	29098	1	2862	

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28924	59292	A	29099	1	1567	MKLNKAGFNVPESYSLMKMP VGCLISALKKAEADRQEVILRLF NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLGPF RVRAGESIKFFNVLLADTPGLDI DTMDKDV AHDSSISQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLEKDLALNQAMIPGSGCT MKLNAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLD AEIARIEKMGVPIKCTTEV GNTLTLEQVKAENRAVLVTVG LSSGSGLPFEHSDVEIAVDFLQ RARQAQGDISIPQSALIGGGDV AMDVASTLKVLCQAVTCVAR EELDEFFASEKEFTSARELGSII DGFTPVA VEGNKVTFKHGDLR TAPFLGVADKRNKSAGNHP
28925	59293	A	29100	107	892	LAICTGTYSGRQVLPFRVDRGA SLIAEERNAGRRRAGIRTTSA GGGLCA Y AIVEF* CWRNCARFE LN/AGISVPI/SEFIGATMQQTVH AEQSAISHA WLSGEKALAAITV NYTPCGHCRQFMNELNSGLDL RIHLPGREAHALRDYLPDAFGP KDLEIKTLLMDEQDHGYALTG DALSQAAIAAANRSHMPYSKSP SGVALECKDGRIFSSEYAENAA FNPTPDIQRAVLAEKADAPLIQ WDATSATLKALGCHSIDRVLL
28926	59294	A	29101	1	3100	
28927	59295	A	29102	1878	2699	GTARNLTVSLSYSSSGTPSNA PNARMEELGPHPEASSLFHPE SPLLDELFLPEYKAGRTNPDI GHYVRRADVADGKSRLRLGLDS NKDQSYFLYTLSEHQIAQSLFP VGELEKQVQRKIAEDLGLVTAK KKDSTGICFIGERKFREFLGRYL PAQPGKIITVDGDEIGEHLGLM YHTLGQRKGLIGGTKEGTEEP WYVVDKDVENNILVVAQGHE HPRLMSVGLIAQQLHWVDREP FTGTMRCTVKTRYRQTISLGPL RKPPHNRCLEI
28928	59296	A	29103	358	1160	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
28929	59297	A	29104	234	930	KRAFLCSFCANRRNAANSALAL PGNCPVAHAQKRHSAPGTLSPD ARNEKQPLYGGAAPETPNRL PPLDSGILGGYIAPDNLITLTSV GHSLFDERFGLAPQMPKKLQK MTRFPNDSLDAAALCHGDVLLQI CANTQDVTIHALRDIKHPTDLL SVRWKREGFISDHAARSKGKET PINLLGFKDGTANPDSQNDKLM QKVVVWTADQQEPAWTIGGSY QAVRLNQFRSVMN
28930	59298	B	29105	1	837	
28931	59299	A	29106	1	1701	
28932	59300	A	29107	733	1323	
28933	59301	A	29108	1	736	MKPSVILYKALPDDLQRLQEH FTVHQVANLSPTVEQNAIFA EAEGLLGSNNVNAALLEKMP KLRASTISVGYDNFDVDA RKILLMHTPTVLTETVADTLMA LVLSTARRVVEVAERVKAGEW TASIGPDWYGTDVHHKTLGIVG MGRIGMALAQRAHFGFNMP/R L*RAPPP*RSRRTLQRLRLFY SVTRVRFRLLPDAVN**DASSV WRRRTIRGPSLGLSPGWNTVRSL CAFFG
28934	59302	B	29109	1	1359	
28935	59303	A	29110	874	1926	
28936	59304	A	29111	1	777	
28937	59305	A	29112	137	376	
28938	59306	A	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGN FC*RHGS*KITAGYIVPLPEESA TATGASWTHPWGRQDASW
28939	59307	A	29114	1846	2126	LMELIEKHVSFGGWQNMVRYH SQSLKCEMNVGVYLPKKAANE KLPLVYLWLSGLTCNEQNFITKS GMQRYAAEHNIIVVAPDTSPRG SHVADADRYDLGQAGACFYLNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMGG LGALVLAALRNPDYVVSFAFSP IVSPSPVWPVWQQAFAAYLAEN KDAWLDYDPVSLISQGG/LRCG NHG*SGVE**FLRRQLRLQI*KD WPQ*EAHVH

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28940	59308	A	29115	184	985	LGKRLVTYHTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEGGVEIEKVAEETPLHIHKVALDPLTGMPYQGRELAFKLGLEGKLVQQTQIFMGLATIFLERDLALIEINPLVITKQGGDLICLDGKLGADGNELFRSLILREMRDQSQEDPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATKERVTEAFNPPGYIGPYQGVPPAGPGVTRMGKSVRRIVQVGCQVAAGSH
28941	59309	A	29116	1825	3186	
28942	59310	A	29117	366	1903	
28943	59311	A	29118	1	2139	
28944	59312	A	29119	345	431	AASGSADDNLHHQYN*GDIACLHALLP
28945	59313	B	29120	1	2616	
28946	59314	A	29121	1	1521	
28947	59315	A	29122	1	783	
28948	59316	A	29123	96	215	
28949	59317	A	29124	1	292	MWWGGLLYWLAALVTLLWAASQIQALKKLTCAISQTLTEEQPVLSKSWLTSQNDYSLPDSLTERJWLTLISQRISRGELREF*TGRRKLVTQECLV
28950	59318	A	29125	3	529	
28951	59319	A	29126	1	884	MVDSLIA RVGV MARGNAITLPVCGRDVKFTLEVLRGDSVEKTSRVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEIGDGSRRRKAALTESDYRLVYGELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLRMKVEEGDVILVKKLDRLGRDTADMIQLI KEFDAQGV SIRFIDDGISTDGEMVLDKLARGYADLSKAESQWDEMMRTAGSLKLGTHASELIRSLKSSRPSGLAQAIMEVGRVNKTYLLNYIDDEDYRRRILTQLNRGEGRHAVARAICYGQRGEIRKRYREGQEDQLGALGLVTNAVVLWNTLYMEEALSWMRRNGEEHDEDIARLSPLMHGHNMLGHYFTLPEDILKGLR*RHLPPSSASPALPIGIHVHKHLLGDNRYPWIMQPSAHHPARQPEHDNHR

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28952	59320	A	29127	143	523	NQTLMIKGAAHGIFNPLCIKAT AGVAGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPLILPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	B	29128	I	4107	
28954	59322	A	29129	1892	2720	PTAWSPPRPTSMTSISWVICCM ERSNLSQPMPTATKGRQARGAG VEVDVDWLIARPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRQFGFVKARFKGLLK NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFALISTA SALAGLILLCLFGPALLAGYITE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRNGRVFLLVFILPFS LRRVGHAAH
28955	59323	A	29130	1332	1635	
28956	59324	C	29131	I	1677	

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28957	59325	A	29132	1	1114	MAEACNIGLEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFTVPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGLTRDSNLFVLEGLLEQQTG LNPVEIMTDTGCGLEKQEEPPS LLRLNNRIKQLLPPVDLTELLE IDAQTGFTEFAHVSSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFTVPVK TINSGSNRKYFGSGRGITWYNF VSDQYSGFHGIVVPGLTRDSNF VLEGLLEQQTGLNP/D*NHDRH LRLSGETGRATIASSK*SDQTA TPTGRFNGTVEIDAQTGFTE FAHVSSESGARAQDLHISLRY* WLKPVIS/ALEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFTVPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGLTRDSNLFVLEGLLEQQTG LNPVEIMTDTGCGLEKQEEPPS LLRLNNRIKQLLPPVDLTELLE IDAQTGFTEFAHVSSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFTVPVK
28958	59326	A	29133	1	2908	
28959	59327	A	29134	735	932	
28960	59328	B	29135	1	1413	
28961	59329	A	29136	1	1469	
28962	59330	A	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	A	29139	1	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNLALL RRFHEATAQNAPDVVWVGSGT PMREFLHVDDMAAASIHVMEL AHEVWLENTQPMLSHINVGTG VDCTIRELAQTIKVVGYKGRV VFDASKPDGTPRKLLDVTSLHQ LGWYHEISLEAGLASTYQWFL NQDRFRG
28967	59335	A	29142	538	1116	
28968	59336	C	29143	1	2967	
28969	59337	C	29144	1	2214	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
28970	59338	A	29145	1	469	
28971	59339	A	29146	780	1052	
28972	59340	A	29147	617	2408	
28973	59341	A	29148	2	488	
28974	59342	A	29149	1	1083	
28975	59343	A	29150	527	3213	SWRSVQLLPATSIPIWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNLKEHGCGVTPIMS MRRWLAKNRPQADVRVINYVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSLGKFTKLQPAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGYAVVALIKPGAQIGR SPVNCDVASCHVISFNLRLVELAI MRRLLCRIAVLMSYRIEQRLMF LERLRHVGLIAHPAKKAIKKTR KPGMKVTFEQLKAAFNRLISR GVDSETADACAEMFARTTESG VYSIIGVNRFRFIQQLENGDIIP DAQPKRITSLGAIEQWDAQRSI GNLTAKKMMDRALIELAADHGI GLRLLAGGGKRLYWHLLDQLH RRNDNISLDLGNNAEAVILRED MLPRENFRPGDRVRGVLYSVRP EARGAQLFVTRSKPEMLIELFRI EVPEIGEEVIEIKAAARDPGSRA KIAVKTNDKRIDPPTQHEDEED EGLYDDPFPLNECSVGPGHRRR FAPPEAQFRRPETLKGAPTSRIP ETSVGVSGSDFEPHLMRELTC RLTAITWCYPGSAYAVHPQDE
28976	59344	A	29151	1	812	
28977	59345	A	29152	1	1830	

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28978	59346	A	29153	1	1308	MMPLIDLEDPRLVLRREIGMLL HVDYLDLVHEKVICRGRNGGQ DREKTTMEKVRSSGTICPQAP VVNHVFTDDGYRIISARFGVP RTQVRTWVALYEKHGEKGLIP KPKGVSADEPLRIKVVKAIVIE HMSLNQAAAHFMLAGSGSVAR WLKVVEERGEAGLRALKIGTK RNIAISVDPEKAASALELSKDRR IEDLERQVRFLERLMLYKELK ALAHPTKKVTLSHREGKQINH KAVQRLMGTLSLKAIAIKVKRY RSYRGEVGGTAPNVLQRDFKA TRPNEKVVTDVTEFAVNGRKL YLSPVIDLFNNEVISYLSERPV MNMVENMLDQAFKKLNPHEH PVLHSDQGQWYRMRRYQNLK EHGKQMSMRKGNCLDNVVE CFFGTLKSECFYLDSEFSNSELK DAVTEYIEYYNSRRISLKLKGL
28979	59347	A	29154	1	836	
28980	59348	A	29155	1	1566	
28981	59349	A	29156	297	936	RTSSSLMRSSSLRLRISGVSPRS IPRWFTSVSLPSSFRITTFRYT PGHVAPASRRSCYKYYR*PMRL YTMQISLS/VGSRPSGLRAFSSD CSPLPRTCSLRRRVLMITTSRS *SLTYGVDPVSRPVLAASEYF SRRVYAGFQNPNNLLVSG*YQG NYRHFGLRGYPG/TLKNSNFQL TRSARISLSSRSISCTSTGGNTTL PPSSPPDC
28982	59350	A	29157	5	861	SWRSVQLLPATSPVQWETNQ FMGRDRPTTAESPYAVLLRP LAKLNIQRPVNMNMVENMLDQ AFKKLNPHEHPVLHSDQGQWY RMRRYQNLKEHGGCVTPIMS MRRWLAKNRQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCCKTKVVSGEYTVSSTMTLT DAEIAEGY
28983	59351	A	29158	1818	1991	SPSHIRRTAFNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPPQGW
28984	59352	A	29159	3	601	
28985	59353	A	29160	415	549	

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28986	59354	A	29161	2	501	
28987	59355	A	29162	1	1347	
28988	59356	A	29163	3	2461	
28989	59357	A	29164	1419	1640	IFCASLSGLGYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPGQC DPHMESLI
28990	59358	A	29165	1135	2067	
28991	59359	A	29166	1	1364	MAGNRRFMCTPKTHGLSISOH GTFPEHAGCKIRCAGRSGRVVRP AELLAPYTGIDIAEGISKAMRG GAKFLHHGIKQQRYVVAEAIT EWRMAPGPLEVAVFAGVIYHL YYYRARFFCAAQPLVSGFHEAE LSLDDAKWVLHPGPDAGFHV DVDGRFVLAWMLFQGSYLAG ALGDQPVHIIHGLQLLALWRPL QITQLIEVMLVGRGDQAVGQ ATLGIDTNGGLYAKGPLIAFLG LMHLRIALLFLVLRGTGCAYDG GRPQLAEKLYSELRAQIEVL DDRKERPGYMFADMEIGIPHT IVLGDRNLNDNDIEYKYRNGE KQLIKTGDIYEYLNALLIAVT VLTSMESDLVDLGMTLSPAD YAERLAALTQKCGLDGVVCSA QEAVRFKQVFGQEFKLVTPGIR PQGSEAGDQRRIMTPEQALSAG VDYMVIGRPVTQSVDPQAQTLK ATNASLQRSA*CRDAGTLRLRA WLC*FLQRRYHRYKGPVFPQV ELCQICQRNEFCTQRPVGMCHV
28992	59360	A	29167	627	854	NAGDRNRNFSCTAARQYGS RFYNCRR*RHGRKNLSAERNGL PEYRNCNPDHRPSVFLAAGRCF APTMCCHDASE
28993	59361	A	29168	1	1593	
28994	59362	B	29169	1	3789	
28995	59363	A	29170	940	1326	
28996	59364	A	29171	1	1377	
28997	59365	A	29172	1	2547	
28998	59366	A	29173	561	845	AKIVQLRPRI LRPSRSARRCP PSRRQRRRSGPLPEPAPRV S*QIFPSQYWR YRQSTENQKQRL DP RGQIVNVPARRIIRQKRCK CKV AGSA
28999	59367	A	29174	1	1284	
29000	59368	A	29175	624	866	
29001	59369	A	29176	1	1384	

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29002	59370	A	29177	2268	2684	RCRRCKRLLRRFRRLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRC HCG* RQC SSDGRKITSVHRGRNADGREL T HQA VRL LAYL SDRFARHHRHL RNAHRRGPDRIKERHFPATKL RHTPAV
29003	59371	A	29178	1	2142	
29004	59372	A	29179	1	2463	
29005	59373	A	29180	3	126	
29006	59374	A	29181	1	2013	
29007	59375	A	29182	891	1000	FDSFHWHSHPMLCCDRGQHK E NPQSRGPISQC*IQQ
29008	59376	A	29183	1	846	
29009	59377	A	29184	90	411	
29010	59378	A	29185	1	1580	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPR TQVRTWV ALYEKHGEKGLIPKPGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNAISVDPE KAASALELSDKDRRIEDLERQVR FLETRLMYLLKKLALAHPTKK AAEIPRSTFYHHLKALSKPDY ADVKKRISEIYHENRGYGYRR VTLSLHREGKQINHKAVQRLM GTLSLKAAIKVKRYRSYRGEVG QTAPNVLQRDFKATRPNEKVV TDVTEFAVNGRKL YLSPVIDLF NNEVISYLSERPVMNMVENM LDQAFKCLNPHEHPVLHSDQG WQYRMRRYQNLKEHGKQSM SRKGNCLDNVVECLFGLTKS ECFYLDEFSNISELKDAVTEYIE YYNSRRISLKLKDL YASCLTVQ LFGVSTVMGLLIRILGSIFQKAL NISKIESFVAVTTIFLGQNEIPAI VKRFMIAESHEVLPHLYGMGH CGSRRWYAEWRPLHRVHEPSG
29011	59379	A	29186	1375	3174	
29012	59380	A	29187	604	1268	
29013	59381	A	29188	1	288	
29014	59382	A	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	A	29192	1	3156	
29018	59386	A	29193	1	1824	
29019	59387	A	29194	1	1922	
29020	59388	A	29195	1369	1743	

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29021	59389	A	29196	21	432	GPGCNGVHRLCTE QRDVRGTV RIVLKFNFNCRDVTFVAFEVNN TVSLLVATTDMTSGDTAIVVT TGFVSAANEVQILAFFQGDVSF FPVATTTDTLSVTFFPNFYQG VNDFFDFKQFLHSSDFCFGR VFSNFE
29022	59390	C	29197	1	1743	
29023	59391	A	29198	2005	2571	
29024	59392	A	29199	170	486	LQTQKDGIPAVVERLEYDPNLP RTSRWFRNDFSVVPLQLLGSP*
29025	59393	A	29200	1	1713	
29026	59394	A	29201	1	6729	
29027	59395	A	29202	1	753	
29028	59396	A	29203	1	1470	
29029	59397	A	29204	665	1773	ASSQVKSGWLSAKIPVISSYGP LLSVRLLSHAWPNLCPQLHCF LPGAIWSASSLLKSGNRPLRLA SIVLPVPGGPISKRLCPAAV/HF QSSLSLFLTDNITEIML*RPDTW THVMYVLHHADKPNLYHGLPE NPEISETVKFWKGIWKPLAAGV FAATFAASIFHYVGVGNRADE EENNLHEEKDEERKCSQDIQLV KERVIFLTGQVEDHMANLIVAQ MLFLEAENPEKDIYLYINSPGG VITAGMSIYDTMQFIKPDVSTIC MGQAASMGAFLLTAGAKGKR FCLPNSRVMIHQPLGGYQGQAT DIEIHAREILVKGRMNMALMAL HTGQSLEQIERDTERDRFLSAPE AVEYGLVDSILTHRN
29030	59398	A	29205	948	1620	

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29031	59399	A	29206	1782	3667	HRRRCRHGYPPVPAAYRCRIWKCGQFHPTGIAGCGRTGHRRLPW*RRLSAEQWTWRTFYGALCAERQRPGGP*RG/SRSIMIEIREGRGCDGPWGPFAKLKLDHLGKEVLESRLPGILELSRTFAHVDPSRFRLSLSLHDGRYSQSYRYNDTRDMVPINGSIHRIGREPHYHYQRCGQQYIGLCRNCNVIDTHICIYLVDPQIMDDIRRLLYSEISSAIHWLLPVVQGEHYMLVDPDTNEREERGRSETRGFPRVPLGRTVSTVWYPLSNAATLAATRCRSRSPHAFAPSSNNGFITATPLGRTHFLGMAFPSPACWRLRAEPERVEAVLSASGMNKAMRCGVSLICNFRLDYAPIEKQWDLHFADYFAEDLKLAPLAKDGLVDVDEKGIQVTAKGRIIRRLRIRHLSMMPDAALVASYQAYDFLRIRHKQASAKQPNHCGTQHGSNGSLRTLWNSIDSGSVLTWCASLIFSSRKSLSPIQLVRSVDRCGDVKKRYSMREFSLGETHSEAEFRELEQNPSFVFFKPQSFAPVKGASAVPLVGRASVASDRSHPPGTTLLAEVPLLNNKGKFNQGYELRLMVALDVGGAIKGQHFIDIYQGIGPEAGHRAGWYNHYGRVWVLKTAPGA
29032	59400	A	29207	1351	1806	VIVGITSNSVTVAAVSSWCRTWVPVSVLCLNCYPASMALVRGVI RGV*TCLSLCPNCAAIIFAFGA VIFCITSVGFLFPPMVYKSGLRF FVFT*MRDTGVPQRLRAPRRSL SAKLGPACPFAYIVPHIWCRIWGWGTCVCLAICVCVCVAD
29033	59401	A	29208	1308	1647	RSWEVSIVFYVVVRPTGHV*HASGNLSHHRKRHPLADQAARKGETVPPRGRS/WRTQAHP*HLRQHRGQHPASL.PTRTGTPQGRRAIYRIPVRTAGQFQRIEVDGFQRVGHQ
29034	59402	A	29209	1	2184	
29035	59403	B	29210	81	1356	
29036	59404	A	29211	1	2349	

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29037	59405	A	29212	514	1136	ILRIMQRMGMKQFAGLLRLSGIK MLPSA**LGELLHAAGSFFQRG CLLFSTGGKIGVARRNFTGTGI DGI*TFADMSDGVSQRALHM* NALRQVAHFAPVNGQGIQV TTGDFANVSNNFCQRSKQHTA NAVPRHQNQYHHQRDNRQLP LGKSVIICVVSDDIAIQFFTAEG VLSKRFAHCLMPSLGLGLSKIGP SMPLFRIISQFS
29038	59406	A	29213	1	2992	
29039	59407	A	29214	1	168	
29040	59408	A	29215	1	537	
29041	59409	A	29216	1	1881	
29042	59410	A	29217	1532	2160	KHWSDSIPGTEADWSASTTSGC AGFAAFACSSS*VICLLSGAVA AYAPQLRHQAIKRVIRRTSAFP LMD*TWFLSSTNGLASCASIS SAGSGAGSASGVTKVSVSDTAS GWPIFVTDLSSCSTRFTLPKAN RLITVEPSLKRPISWPFSA TEPS FSPAGQVQRLMIPSRGGVMVP AQTVMSLPTIVATPGPYSHLL GSFTLSPP
29043	59411	A	29218	1	1713	
29044	59412	A	29219	2159	2715	TIPAKPVPSMVASGTVRFGFLT PVLTAADSTPTKAHRQSRILLMI A*PSVVS AVFLAA*VAASNQC QPTIAVITTGIRTSTRPIVA/CITG FVTGA VEIVLVANSVIDISVGSP FSIPQMFSARLGIATMAICPIMV SFSVAAINSASHNRQGFALQFFF NDAACGSGEFRILMQEEHPDSV VFC
29045	59413	A	29220	2	102	DFADFGTTIKQDFRLLGQTSVD RLQLSQGQAVKGNQLLPVSL VKRKTTLPNTQTASPRALADS LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM SVDLCHRDFAFGTTIKQDFRL LGQTSVDRLQLSQGQAVKGN QLLPVSLVKRKTTLPNTQTAS PRALADSLMQLARQVSRLESGV IGGAGSLAFPLPALIWCAVRYT PQVTCLLTFVTGILPISEPPSNRI FACWGKPAWTACCNLRARR
29046	59414	A	29221	1	1464	

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29047	59415	A	29222	3	29	MQTEQQRAVTRLICQGLFLL QHGAESALVDELSRLGRALG MDSVSESSISNAIVLTITK/D/GQC L.TSTRKNHDRGINMHVVTEVQ HIVI/LAEHHLDPPEP*EQQRR
29048	59416	A	29223	5	307	
29049	59417	A	29224	5	948	
29050	59418	B	29225	1	696	
29051	59419	A	29226	1	1083	
29052	59420	A	29227	817	978	LAGCYTMLPGNGPAGMHACIS KLDK*A/VKKRISEIIHENRGY GYRRVPLSLH
29053	59421	A	29228	198	362	
29054	59422	A	29229	1	2907	
29055	59423	A	29230	1	2541	
29056	59424	A	29231	1	1566	
29057	59425	A	29232	3	601	
29058	59426	A	29233	1	1347	
29059	59427	A	29234	940	1326	
29060	59428	A	29235	1	2547	
29061	59429	A	29236	527	1383	SWRSVQLLPATSPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNILKEHGGCVTPIMS MRRWLAKNRQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFTPVAAEA TSGLKFTKLQFAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCKTKVVSGETVSSMTMLT DAEIAEY
29062	59430	A	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	A	29239	1135	2067	
29065	59433	A	29240	1	1566	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29066	59434	A	29241	1	1605	MKVPRGDMVFMQLNRKDDGQ FEDQLLLVLLPKHRGHLLQV ADDVWFKNNRAKCRQRRQQQ KQQQPPPGGQAKARPAKRKAG TSRPRSTDFRSRDGIPEKATRTS CPSDSSVSFLQRPLSSTGRGSS LSWDSSQVLVILSTLTPSGTIVT AEPKYPFKEKLEVVNHVFTTDD GYRIISARFGVPRTVRTVVAL YEKHGEKGLIPKPGVSADPEL RIKVVKAVIEQHMSLNQAAAH FMLAGSGSVARWLKVVEERGE AGLRALKIGTKRNIASVDPEKA ASALELSKDRRIEDLERQVRFL ETRLMYLKKLALAHPTKKVT LSLHREGKQJNHKAVQRLMGT LSLKAIAIKVKRYRSYRGEVGQT APNVLQRDFKATRPNEKVVTD VTEFAVNGRKLKYLSPVIDLFNN EVISYLSERPVMNMVENMLD QAFKKLNPHIEHPVLHSDQGWQ YRMRRYQNILKEHGKQSMRS KGNCLDNAVVECFGTLLKSECF YLDEFNSISELKDAVTEYIEYYN SRRISLEKLKG/LTPI
29067	59435	A	29242	3	1119	
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRRIEI SIEAGRVSDDGEIAKLGDNVE AWYRRLAGAFTLQECVMAA STFFIPSVNVIGADSLTDAMNM MADYGFRTRLVTDNMLTKLG MAGDVQKALEERNIFSVIYDGT QPNPTTENVAAGLKLKENNC DSVISLGGGSPHDCAKGIALVA ANGGDIRDYEGVDRSAKPQLP MIAINTTAGTASEMTRFCITDE ARHIKMAIVDKHVTPLLSVND SLMIGMPKSLTAATGMD
29070	59438	A	29245	104	1381	
29071	59439	A	29246	1	375	
29072	59440	B	29247	1	5082	
29073	59441	A	29248	119	343	RMPKRRRWGKLSTIRCSSTTCKK RLT*IVLPVRTPGRLCSSLSKSV ASHCLASCKAYSINKPWRQPS KRHYVTMR

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29074	59442	A	29249	468	935	VPLAVPYGRLWRTIFSLPSSFR STRVR*EVSGRSSPSISLASLVR PIT/SLIVNAHPVELLQVVFP TL DKHIAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPT E AVDLFFHFNAVTGFGHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	A	29250	407	2145	
29076	59444	A	29251	1	177	
29077	59445	A	29252	1	1767	
29078	59446	A	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	A	29255	2	314	
29081	59449	A	29256	2977	3913	
29082	59450	A	29257	1	2091	
29083	59451	A	29258	1	751	
29084	59452	A	29259	1	927	
29085	59453	A	29260	1	1113	
29086	59454	A	29261	1	875	
29087	59455	A	29262	1	450	
29088	59456	A	29263	1	522	
29089	59457	A	29264	1	912	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29090	59458	A	29265	1	2416	MLAQLSLQALEQDGLFNRIAYPV VPPHVEYSLTPLGEQVSEKVAA LADWIELNLPEVLAVRDERTRY DIAVPRKRYGHAVSRNTFALRS QERYGHSVLETVGNSGSSKQFS MDILDPCARGPGQISLITVNHKL HVRCEIAYSVQTMVVKGGSA FAAFFIAVVLWMIGYVPNVEQS TQALLGMQFIMIALPTLFFMVT LILYFRFYRLNGDTLRRQIHLL DKYRKVPPEPVHADIPVGARLS FAERVMEGLSDGGQSLQSPSAL FSKQTLKNMSIYKIPLPLNILEA ARERITWTLNTPRVCSVSGG KDSGLMLHLTAELAROMGKKI CVLFIDWEAQFSCITINYVQSLR ELYTDVIEEFYWDALPLTTQNS LSQYQPEWQCWEPDVEWVRQP PQDAITDPDFCFYQPGMTFEQ FVREFAEWFSQKRPAAMMIGIR ADESYNRFVAIASLNKQRFADD KPWTTAAPGGHSWYIYPIYDW KVADIWTVYANHQSCLNPLYN LMYQAGVPLRHMIRICEFGPEQ RQGLWLHYHVEIPDRWAAIGSP ADREEDAEEYLEAIMEARVTV AGMGLVMEVQDYFDGEA'DRL AKAWLP/EYTPQIKSLKDERKE AYRQIVEMSTEPQDQDVLVRPA NKFEMTRVREGEKEADLPVWK HLLCDESGNYPALLNHWETK VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	
29092	59460	B	29267	1	10161	
29093	59461	A	29268	1	882	
29094	59462	A	29269	1	2484	
29095	59463	A	29270	548	945	
29096	59464	A	29271	17	352	DLQDTGCFMLMNTGEKAV/KS ENGLLTIIAC/GPTGE/VNYALE GAVFMAGASI/QWLRDEMKLIN DAYDSE/YFATKVQNTNGVYV VPALPGWSLLWTRTCHRIFFRH RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIHELN TDFLCLINHVVGGHIAFTGVD DDTGA*TFEGLCLIR
29098	59466	A	29273	1	975	

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29099	59467	A	29274	65	562	DFRWHGDSRKVHRKNRLIKPL MILLTRLNRTNWPLTAAVIWP GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSTSS SIHHHINSSSLQCQPCASKYLAH YFTVSSIAAYSTPVVSTQEPWA TRHHPHHQQTDRRRPATRKSPR QYHNETNRQ
29100	59468	A	29275	1409	1641	PENGRPVYAGGRDAAWRDYY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSA LGLCL* RLAGGDWCRDYSL
29101	59469	A	29276	1	3252	
29102	59470	C	29277	1	2760	
29103	59471	A	29278	1	723	
29104	59472	A	29279	14	338	
29105	59473	B	29280	1	1201	
29106	59474	B	29281	1	1866	
29107	59475	A	29282	1067	2753	
29108	59476	B	29283	1	1144	
29109	59477	A	29284	3	724	LAQLYGDPPAWPTPTRGVSEIR LALRFKSNDSLRLRHFKDSTLY LEIVDYPGEWLLDPLMAQDY LSWSRQMTGLLNGQRGEWSA KWRMMSEGLDPLAPADENRLA DIAAAWTDYLLHCKEQGLHFI QPGRFVLPQDMAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL Q/PLNSGHSIYDMR WPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	A	29285	1	1863	
29111	59479	B	29286	1	813	
29112	59480	A	29287	1	546	
29113	59481	B	29288	1	2691	
29114	59482	A	29289	1	1212	
29115	59483	A	29290	1	2328	
29116	59484	A	29291	1	531	
29117	59485	A	29292	188	358	
29118	59486	A	29293	2545	2713	LLVVQFFQHL*VPSGTSP*L*H LSGILWHFLQLALLYRPFVLV LCRSLGAVCLY
29119	59487	A	29294	1	2046	
29120	59488	A	29295	3	654	
29121	59489	A	29296	2	182	
29122	59490	A	29297	1	1215	
29123	59491	A	29298	141	266	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN ASGHAQRQSDGDLRSRAATGG DHSAGDWCGRRVQTSAG*LWR KARPWPNR
29125	59493	A	29300	2353	2758	SQAYHQVLPVCEAAPIPDDNHT LAALR*HGVEYEHMDQDCWA SFLPEERLFWRPIAPRSDRVEC VDSLPLTAVGKVDKKQLRQWL ASRASARAQRSSPLAEARKPQY VHQGMDNARTALQKPEQARA HTEVHWT
29126	59494	A	29301	5	793	FLQRFVADLPCGAQVVKFSTFR TQCRQTEATLKVLFHGTFTNVV TSIGATTQVTNDARTDLRKQLV IDILFGIRRTLLHFLDRHNRHF CRCRSRNTFLFQLLRMIRDFND FELV/NPLSLDSVLGMQPLREEI QQADRDDDKHHQGAGLLELET ANRFPQGDADPACADHADDGR RADVGFEAIEGVGDQQWHHL WQHAVEDLFELVGTGGANAGP GSIASSTESSLESTPVVWNSA STPARQRTGRGRRRPTAWRRP
29127	59495	A	29302	1	2457	
29128	59496	A	29303	1	292	
29129	59497	A	29304	1	440	
29130	59498	A	29305	593	864	RTSAEPINPAPPVIRIFLISARLC* WTLSPILTLN*L*STSITSTSAVA SASSSCARVQSPVSFFGNWWM LGSTTRVSPLCHWAISSADF
29131	59499	A	29306	2	696	VPAGRYTGRDLHLHL/LPFRS LPARHRVRRYRPLEAC*TPCTD GYHRIFYRLKGESAKDGSVMT LRSFLDKDGHPIDVEDINDQAR HLVRLMPVLRRLRDARFMRRIR NGTVPNVPNVEVTARQLDFLA RELSSHQNLSDGQIRQGLSAM VQLEHYFSEQGAGQARVRLM RRRASNEQSRWRYLDIINRMD RPGGRSYRVILLGLFATLLQAK GTLRLDKDARPLLEIE
29132	59500	A	29307	3	1405	
29133	59501	A	29308	1204	1411	LRPALYQPARLSDAAVRKTG*F AVVSGSEHAESDAG*SGELLEQ LSEVLR*PDEIFLWRCRAEREQL GL
29134	59502	A	29309	236	645	

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29135	59503	A	29310	1	776	MELAAALRSENQPQDEKPLGETL KDLFSRPVLPMTDVHLPNLN IEEFMGEQLHVTGDTDIYREHH AAEMSNIDGNTKLDALDISSQ GIVDASGTAHLSDNWVPVDITLN STLIVEPLKGDVKLKMGGAL REQLEIGVNLSPVMDMLRAHT RLAEAGLSLNVEVNSKQLYC/L AHCMSMPKESGADEKNSDNR WCRVYWLGAALYHQRNERR GGSGR*ADLRKPDVAGTGRA KRALCL*ES*YLRSGRTGTRIH
29136	59504	A	29311	955	1095	HRRHPIPLIHHRDQPFRLQLRK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	A	29312	1029	1490	RLPPAVDPTARLRPASGRYP CIPAFVGTAPVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWSQLDRQANPAQVEIIEIRQ LVRKSPQTAHSPARIWRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSQKYQSRARRRPAASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQL SLSDKCRQGTVSGRLSLRKSDC TPISHASCSSSLHGH*VSVAVR LRMTDFSRVTGKDQVRFDAGL GWTLERLLSAAAFRVALKAG DMAILASRPPTVTTPNSMRLGR LYRSGVYGR

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29139	59507	A	29314	2	2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWGYDYTGADN NANFGKAVPADFNNGGSFGRGD SDEWTFGAQMEIWCYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRCGAKSPFCAIT FRVRWTIRKSTKCCANRAYKR NITVGRIRRLRRIRQPLPDATLC VLSGLQTEHNRRWPNVSVCHFSP DSTFYNDLSGRMKNVRLMFNG IHRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVEIVGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLLLSPESDLYHFERDD FWFPFGDINGREHHLHIILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFYRLEGESAGEDSVMT LRSFLDKDGHPIECRGI*PIKAR HLVRLMPVLRLRECPVLMRR IRINGTVPNVPNVEVTARQLDF LARGGQARYRLMRRRASNEQR SWRYLDIINRMIERPETRYTREI GFTSTNIDLIYGLPKQTPESFAF TLKRVAELNPDRLSVFNVAHL TIFAAQRKIKDADLPSPQKLDI LQETIAFLTQSGYQFIGMDHFA RPDDELAVAQREGVLHRNFQG YTTQGDITLLGMGVSAISMIGD CYAQNQKELKQYYQQVDEQG NALWRGIALTRDDCIRRDVKS LICNFRLDYAPIKKQGDHFD YFAEDLKLLAPLAKDGLGDVD

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29140	59508	A	29315	1	2237	MLTGYRAVSRHKSQRYTADDA EEMIGKLTGMPIPLNSLRQWIL GLPGDATDYKLLDDQYRLSEITY SQNGKNWKVVYGGYDTKTQP AMPANMELTDGGQRKCLKMD NWRADGYHTLQTLFQFLDYG DTISIELRDDGDIRLLTPVEGVE HEDNLIVRAARLLMKTAADSG/ LSSDGKR/RSSSCARVQSPVSFF GNWWMLGQTTRVSPCHWAIS SAISHRRFAFAQVINIRFKRQTKA GDFQFTGAFIGSRQAISHRRFHL IDNPERFVIVHFARGTDKPRLLG VLCHDKPRINSNAVTAHARAR LKNINARVTIRQANQFPDVPNLI GTNQRHFISKSDIHIAEAVFEPSI IAADRLNPLVNELIIMPDIKRL DAFVRIAHEELLYLLGILMNP NKDHVLPILITGPKESADYFRV LDEFVVTLGENARRHYRIIIDD AAEVARQMKSMPVKENRR DTGDAYSFNWSMRIAPDLQMP FEPHENMANLKYDPQPEVL AADLRRAFSGIVAGNVKEVGIR AIEEFGPYKINGDKEMRRMDD LLQGFVAQHFGSYNDLLMEL LPHLLVEGMLISA VSAESLPWL HLSVCVANISKRQLICAVPLPKPP KAGLLGKNIMGTGDFELFVHT GAGRYICGEETALINSLEGRA NPRSKPPFATSGAWGKPTCVN NVETLCNVPAILANGVEWYQNI
29141	59509	A	29316	1	2892	
29142	59510	A	29317	19	649	
29143	59511	A	29318	2471	3036	KVTWVTCISLPMTLSPSAAFSSL FRMKILSLK**KRILR/SSGKPAA RQGDMTQYGGSI VQGSAGVRI GAPTGVACSVCPGGVTS GHPV NPLLGA KVLPGETDIALPGLPF ILSRTYSSYRTKTPAPVGS LGPG WKMPADIRLQLRDNTLILSDNG GRSLYFEHLFPGEDGYSPQRVT VACAPRRGKTG
29144	59512	A	29319	1	1476	
29145	59513	A	29320	688	1578	
29146	59514	A	29321	1	1653	
29147	59515	A	29322	1	218	MLIVFSLPSDTLVLSPL*PNFRT RPFPPSSVPR**PKDKLKIATSA MMEAAYSSVIANVVLVPVMDA KWLAR
29148	59516	A	29323	3	260	

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29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR WLGHDKRATLLWLKLEAAGSP LRPLSVQVTTTQVEAETDNHAD NSYNAGLFIVNSLYTAEGVMD KHSLWQRYVPLVRHEALRLQV RLPASVELDDLLQAGGIGLLNA VERYDALQGTAFTTYAVQRI GAMDELAAAVTGCRACDAT RVKWHRRQ*GNWSRNLAKPR KLR*RVN
29151	59519	A	29326	1	2349	
29152	59520	B	29327	1	747	
29153	59521	A	29328	275	729	
29154	59522	B	29329	1	2469	
29155	59523	A	29330	1	969	
29156	59524	A	29331	148	1180	
29157	59525	A	29332	56	170	VHA*GSLFFPELSMHQDLSQGH EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	A	29334	482	765	
29160	59528	B	29335	1	1713	
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNT**A SAPGN/ARWNSYVG*KHH/SCQ WGDYRRQCFRGE
29162	59530	A	29337	1	3189	
29163	59531	A	29338	1	1344	
29164	59532	B	29339	1	1233	
29165	59533	A	29340	1	1572	
29166	59534	A	29341	1	3591	
29167	59535	A	29342	1	843	MNYSHDNWSAILAHIGKPEELD TSARNAGALTRRREIRDAATLL RLGLAYGPGGMSLREVTAWAQ LHDVATLSDVALLKRLRNAAD WFGILAAQTLAVRAAVTGCTS GKRLRLVDGTASAP/GGGS WRLHMGYDPHTF/TDFELTDSR DAERLDRFAQTADRIADRGF GSRPECIRSLAFGEADYIVRVH WRGLRWLTAEGMRDFMMGFL RGLDCEVPDPKRRTNLSLWITK MVIWSLQVAIRGTVSLTAYKTQ LKNARHRLNEAPRRRLQMVQ PLS
29168	59536	A	29343	2	3203	
29169	59537	A	29344	227	634	IKTLPLSPDKLTRISKSIYRKQR AALFTHSFTTWVLAILEHRRFF AK*TRSISKAHVISCVAAGHTLA AAPQPHYFTRETYSPERVSTLM TSPICTNSGTLTAPVDRVAGLP PVPAVSPFRPGSVTSSSTKFG

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29170	59538	A	29345	1	1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRLPEPPFH
29172	59540	A	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRLPEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTGSPGHRGKPGT REDEHGV/ELDRRLNFEWWK PEYGINLYQDYKQDGFVEIPD QNNPSLGDVMVIMQIGQNVVPW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGVFHR FAVDSYPEAIRALSSQVDGFKE YMQSEIGSRSKFAIFVDGVNNG HHEEEKFKCAKEIRVPIPTGSK TGGLFQVVVLGAIMVAIFYTG GASLALMGTMSSSLFMMGGA MVLGGVMQMISPPQGWNRNFEV QSSKNKPSYAFGGAVNTTGGGI PSPGPVWISRRWRNFLSRFLC RGYELKLTRLARVFFRLYNST
29175	59543	A	29350	1	8043	
29176	59544	A	29351	1	876	
29177	59545	A	29352	2020	2224	CVESRCCHATRCGSK*YSGP/PE DTDCLKTEAAGAGVACDAAEAP DEAPPAKLHVLPPHPEVLKITI
29178	59546	A	29353	1	2346	
29179	59547	B	29354	50	340	
29180	59548	A	29355	284	520	
29181	59549	A	29356	2	304	
29182	59550	A	29357	79	177	
29183	59551	A	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHRHHWH/GNRE NKVNCQLICVDIINTAQPTSES /DQRQH/TLRRQTRDRRHS HEP
29185	59553	A	29360	2	388	YTVSFLLVITQLGFCSVYFMFM ADNLQQMVEKA/TRDLQHLPA QGDSADPHPGHSFLHADNPA LPDPVGVYPEPQGA VRLLDIGQ HHHPWEHGS DL*VYHGGDSIS QQPTLDGKLEDLLAVLYSHL
29186	59554	A	29361	467	3014	
29187	59555	A	29362	1	1174	

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29188	59556	A	29363	1	986	MKVTFEQLKAAFNRVLISRGV DSETADACAEMFARTTESGVY SHGVNRFPRFIQLENGDIHPDA QPKRITSLGAIEQWDAQRSIGN LTAKKMMMDRAIELAADHGIGL VALRNANHWMRGSGNGWQA AEKGYIGICWTNSIIVMPWPVP KECRIGTNPLIVAIRSTPITMVD MSMIKHTLPQRAAGTDRKLAM SREAQLLERHGYAFNELDLGK REPVTTEEKLFVAVCRGEREPV TEAERVWSKYMTRIKRPKRFH TLSGGKPPGKKIVIRPLPGLPV IRDLVVDMGQFYAQYEKIKP/V PVE*WTKSASSRAFTDARAARK
29189	59557	A	29364	99	375	THQPARRFPAYHYAHAAAAA PGDPLGADLQLCARHYHRQRH CVPRHAGYPRSDGLHPQPRGR WRIRCSDCLRVP/SDRGDAGDY FHL*LADR
29190	59558	A	29365	871	1206	
29191	59559	A	29366	1784	1966	RPLDVSFMSSTNSPLTDLVG YLTFSAIFLSWRLLSLLDAA*TP YPPWGSVHCRRFCSL
29192	59560	A	29367	1	1276	FHIKLVLTGATWTALPYCHSHV GLRASLKPTPPFWGRAPLGTRP SQQKTECRILNFPETPIFGNSFK YDIEVSNKSPDEEVKLRHHHLA RCMKNFKTDIYFVSTFEPSTKS VDLLTVETTFAGTVCEYADMPK EWTTTTRGLYDPHTLISASCHKV EGLFSFEDRTVA TLIRLFIHPVK SMRIGLTHALADVSGLAFDRI FMITEPDGADIAVKTFTGIRLKV PCPPDHPAFSITNHQTEVTALV VFECDIIVRGSDRLRLSPGGG SNTDWVIFGLLIKENPGSLLAV GVNLLGKILLSVVAASVSESGQN FLSVLPVRSEGCFVVIDVDVEL PGLRDIADSVKTVGIATVPAVIP ALWEAEVDVNIAAFRSQKAYIS GQVNSKSGQQAINT/DATDYSRG HQLKLCLQSECFHGIYHRIDVA

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29193	59561	A	29368	1	1815	STLEDPHYVHIAEVSPPVVIISIY GATGEKYGFITYRCSEHAALSL TKGAALRRKNPSFQLSYGGLR HFCWPRYTDYGYFELQINRLAL FSTNVTAEPTPYMHLAPPVGTQL PLPHLSHDNSSKNSGGCLPGAS VSCNYREPAVRLALASTPLLR AQSPFFMHKDKDPLFWFLTVP KWRKGEVILSSRPKKTEGSW FPKTFFGFGKSHVLVKEFYNRK HHIAKQQAHAVERTRLEFCPKG LGYSKPQTQGDYAIQHF/L*T NLPTGCWAKYA VISFMRD/TV DDKHWP EEHLAKN*LGLLADS GIRV/KLPWGAPHEEERAKRLA EGFAYVEVLPKMSLEGVARVL AGAKFVVSVD TGLSHLTAALD RPNITVYGPTDPLIGGAPENG DSDSALYRLRKEMEEFHLVVG SDIFGKHQHGTE DTSTTCPSTLE EFETQWFITGGINRILLATDGD NVGIDDPKSIEMVKKQRESGV TLSTFGVGNSSNYNEAMMVRIA DVNGNYSYIDT LSEAQKVLNS EMRQMLITVAKDVKAQIEFNP AWVTEYRQIGYEKRQLRVEHF NNDNVDAGDIGAGKHITLLFEL TLNGQKASIDKLRYPAG
29194	59562	A	29369	3	1993	
29195	59563	A	29370	1	1782	
29196	59564	A	29371	1	3858	
29197	59565	A	29372	1	705	
29198	59566	A	29373	104	471	LWWAGA/SYLCWWMGYQMLRG ALKKEAVSAPAPQVELPKSGRS FLEAIHYFGSVFSLFVGDNVGTT ARWGIFALIIVETLAWFTVVAS LFALPQMRRGYQLAKWIDGF AGALFAGFGIHLIISR
29199	59567	A	29374	50	620	
29200	59568	A	29375	194	767	LWW/AGGLYLCWWMGYQMLRG ALKKEAVSAPAPQVELAKSGRS FLKGLLTNLNPNKAIHYFGSVFS LFVGDNVGTTARWGIFALIIVE TLAWFTVVASLFALPQMRRGY QLAKWIDGFAGALFAGFGIHL IISRLALIVPGLLQKNGGWRRM AHSAVIALVCHAIALAEARILPDG DSGQNLSELLNVGSLVS
29201	59569	A	29376	1	1038	
29202	59570	A	29377	1	513	
29203	59571	A	29378	485	1166	

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29204	59572	B	29379	54	275	
29205	59573	A	29380	2	215	IFLLLLPPHHLLLLLLLLLLLLLL LLLLLLLLQ/MIPLEFCRLYRKQG CICFWGSLGEILLMAEGEAGAS PSH
29206	59574	A	29381	100	393	FLLLLLLLLLLLLLLLLLPLLL LFSSSFLLLLSSFFFLSSFSFSF SFSSSPSPSPSPSFLLSSFFGV ISLDVVTLAWQSARITGVSHRT
29207	59575	A	29382	264	911	ILGFLRDGNFWRKSSQSFPPVHH LLICLLRKSSETMQLTDEHLIHD HPKRPPITELVVPGLHEHLRSN VG DYRCEPPHLTKRNIFCILSEA TDITY*LTSSIFPGFCRLT*LLPL TEITGEAVVQPIKFCPCMCFQFS CAKIWTRGMQWHLEAWRCQK PQSPKGGVMTALAQAEPKSGLLE GQFMPPMPQYLAVQKKVVVF DVSVDSEKLVNVRVYG
29208	59576	A	29383	1	261	
29209	59577	A	29384	3	195	
29210	59578	A	29385	1	399	LERLSAPCISLLSRSLSSLSLSS LFFFFFFLLLLLLLLLLLLLLLL LL/SPPPLLLLLLLLLLLLLLLLL LLLLLLLLLLLLLLDPPGDTIQGA PSRGYHPRDTIQGAPSRGHHPG DTIQGVPSRGYHPGGTIQGA
29211	59579	A	29386	15	159	SPLHLSLV*VKQLLLLLLLLLLL LLLLLLLLLLLLLLLLLLLLLLLL LLLLLLLLSSSFLPS
29212	59580	A	29387	17	429	SFFFFFFFFFFFFFFFFFFFFF/C LLLLLLPLLLLLHRRKHLCVTLG CLRWLGLQCVRLQGSCAWLQT LGWVHTYACVCTFFLDQQVAG RILLVEDPRSSLQCCLLLDA/P LCCRFQKNMHFIRT*R*VHCSGI TSIQFNLEP
29213	59581	A	29388	3	282	RELLRGGNVYIGP*SILSFFLLLL LLLLLLLLLLLLLLLLLLLLLLLL LLLLLVN*GVCCTLLSGPEISCRS DFAQGPTPLQGAPQTALGNLAS
29214	59582	A	29389	3	264	
29215	59583	A	29390	296	421	
29216	59584	A	29391	3	210	
29217	59585	A	29392	1	252	
29218	59586	A	29393	1	1731	
29219	59587	A	29394	1102	1362	NLGTAA TLFFLFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFLFLF L/VPLLLLLLLLLLLLLSSSSCSP PPSSSLEKLYLSI
29220	59588	A	29395	3	2368	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, /=possible nucleotide insertion)
29221	59589	A	29396	1	318	MEKKSPAYFCCRDQMQUIHSDA ALQRLTRFNDPEGWSNLAKN QYLSTSMKQKIWQRLASHRKN NPKADSDAYETSDMILSELIS HGEVDDQMLLNATALIRSDDW DFLESALISWDNLPAVVLKELQ QNTPRNDIWAKFFLRQENSSRA QVDEALRVYYALDPDALAQLD VLAKRPYKTAAFRGEKTHRPV RRSVRQNIIDQADRLHGAQRLV INTNRTRVVDQLIEFLHHQHVN AHLAEIVRHHQPNRAGTSDRHL NAMVNSRLDVRNNEQTEYKTV RGLTRGLMLNMLNKLDSTSP CRMLVCCVPRAPPNPGLNPR AHSLNRSPP*NPLKLLSPTGPFEG MRPLGTHFWGGIGHGQGPWEG PQFGLGMNLLVKS LGHWATW VLARAKILRFELGASMMVAST
29222	59590	A	29397	2	4002	WQE*VHYIWGVMMHGDGISMK SRIPVWEEFVPRFQATLELGV AMIFATAVGIPGVGLAAVKRGS IFDHTAVGLALTGYSMPIFW GMMLIMLVSVHWNLTVPVSGRV SDMVFLDDSNPVTGFMLIDTAI WGE/DHGTFMGAAPIRILPAYG LGTIPVAGFGRMTRSSMLEVLG EDYIRTARAKGLTRMRVHIVHA LRNAMLPVVTVIGLQVGTLLA GAILTETIFSWPGLGRWLIDALQ RRDYPVVQGGVLLVAT
29223	59591	A	29398	187	1710	
29224	59592	A	29399	1	791	
29225	59593	A	29400	353	646	FYWNWVPFTNWQNPRLMGQK *HARWLHLRSLLPAM*ATLL*R ENNR*LLLLTLTSIFKTRIRRLS VSKP*VKAKKKTRLIIWSTSKFL SCMMLKFT
29226	59594	A	29401	406	1023	
29227	59595	A	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLIEKMRES GDIHSHHGWHLHPDHKAGFSE EQQA1WQKAEPLFGDEPWVVR DSPGYFALMVRKFNCCVIVFR R*AQRHRYTDVVVEIACRIKR VAALA
29229	59597	A	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	A	29406	1973	2582	

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29232	59600	A	29407	1	1483	MFVLADFGHTRRTRNSRLGHNIL PARIAPDAINKWLSGFFSREVQ LRWVGPMQTRRRVKRHNTVPLS FADGYPYLLANEASLRDLQQR CPASVKMEQFRPNLVVSGASA WEEDRWKVRIGDVFVDFVVKP CSRCIFTTVSPKGGQKHAPAGEPL KTLQSFRTAQDNGGGEGEARA ANTGATHRGRHRSFSAVRYRD RLNMYVLRMDLLYRVKTLW AALRGNYHTWPAIDITLPGNRH FHLIGSIHMGSHDMAPLPTRL KKLKNADALIVEADVSTSDTPF ANLPACEALEERISEEQNLQ HISQEMGISPSLFTQPLWQIAM VLQATQAQKLGLRAEYGIDYQ LLQAAKQQHKKPVEIEGAENQI AMLLQLPDKGLALLDDTLTHW HTNARLLQMRAGGWSVKEG REKEYFQSPRGWGRSLMPSLGI IIRPP*KKPKNTENRRCISAVTS EKEAPETINQYKAAVRRPFLFL ATALAQSEVRVCIWNTN
29233	59601	A	29408	2	1406	
29234	59602	A	29409	1	1818	
29235	59603	A	29410	441	583	GVYRFPWFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPLGSS VSSR
29236	59604	A	29411	835	1143	RQLPVSLYVRAVAFENGCFGSC SVGG*GPPAARLGEEQVRGGSS SPCIARPRRLHSFLLLLLLLLLL LLLLLLLLLLLLLHLSSSSSFSST SSSSCSRSFM
29237	59605	A	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	A	29414	1002	1145	GVYRFPWFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPLGSS VSSR
29240	59608	A	29415	2	289	
29241	59609	A	29416	1	919	
29242	59610	A	29417	329	405	
29243	59611	A	29418	48	268	
29244	59612	A	29419	2	4625	
29245	59613	A	29420	1	867	
29246	59614	A	29421	1	684	
29247	59615	A	29422	409	543	
29248	59616	A	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	A	29425	3	202	
29251	59619	A	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH S

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29252	59620	A	29427	1	1774	
29253	59621	A	29428	3	184	MSENMRCLVFCPCDTLLRMMV SSFIHVPPKDMMSIFSICLSAASI SSL*ASVCSYPSLNF
29254	59622	A	29429	667	834	
29255	59623	A	29430	1	738	
29256	59624	A	29431	39	230	QMAQHLPHLVFGSHSGSLWEL LSH*VYLLILSLPPPHITPQQAPV WDVPLPVSKCSHCSIPTYK
29257	59625	A	29432	985	1205	IPGSRGKNWVVVTGTGGCHRG PAESDGPAGGARHWEQPPA*Y LVFLFCSQRRWPGRQQRQGS RSWPSVRAAP
29258	59626	A	29433	339	592	PLQAWGPSLCS*AGTPSRKPSP STAHVKKHRLCIPTRRGFSSDN WDPVSSPTCNDAQLHAQVDL EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFQLHPCPFQGS*LLCI GLAHAPLAQRSLLSLTF*CLLS IHQTHSPSSFCPLLARSCDPLEE KRHSGFRNFQPFCSGFSS
29260	59628	A	29435	517	603	
29261	59629	C	29436	1	1188	
29262	59630	A	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIIEGSLVLFHWSISLFWYQ YHAVLVTVVL*YSLKSGSVMP ALFFWLRLDSAMRALFWFHMN FKVVSNSVKKVIGSLMGMAL
29264	59632	A	29439	1	1308	
29265	59633	A	29440	162	377	YSHCSIYTRKIQFLCCPSIKTHL GTNLTS*TFFT*VNIISIYLEASLF FSFLDLGRADKGSSTLTVRSIIT
29266	59634	A	29441	1	480	
29267	59635	A	29442	731	850	
29268	59636	A	29443	531	845	
29269	59637	A	29444	11	649	
29270	59638	A	29445	1	2433	
29271	59639	A	29446	1247	2420	
29272	59640	A	29447	29	94	
29273	59641	A	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGRRSSSTSGKGTAGCPQSPCF CRCSTLRRTAASPGISPPCPKICS CSPLESIWMSNGLCRSCPPSEDS TCGC*GCCCCCCCCCCCCCR RRCPSLGS DAGTELETQRPAG TGPPTVAPATFLQSRRLMVGA GTPTLGVRTPGFGLQLGFFYWL EDVERDTS
29275	59643	A	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

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29278	59646	A	29453	1	599	
29279	59647	A	29454	1	504	MWNCLETNKLFFQESLQKTATR LSAFSWEEAKVQLSWVVLNLA TSAMLPKFYPNEIKVTYLRCTG DEVGATSVLAPKISPLGLSS/VK ALKEPPRARKKQKTIKHSQ/NIT FDEIVNVAQHMWHRLSARELS GIIKEILGTPQSVGCNVDGCHPH DIIDDINGGAVECPAN
29280	59648	A	29455	1	1269	
29281	59649	A	29456	434	655	PFSSPASSSGR*KTTSPFAKLFN ACRISLLASAEVNPNISAYLAT WISQIPSCSCLVPDFLIWSTNR YSIRF
29282	59650	A	29457	1	801	
29283	59651	A	29458	2	722	GRVGGGGQGANYLRVVPESGV YSTPSRLPPLPPKVRPPTRFKSV YLEVAPKGEVGAITSALGPQRI GPLGPVSKKKLGDDISKA/TG\ DWKGP*GITVKLTIQNRQAQD *GGCLSASALIILKALKEPPRDR KKQKNIKHSGNITFDEIVNIFAR QMRHRSLVARETLWNHLKRSR GTAQSVGCNVDGRPHPHDIIDI NSGAVECPAVSDIFIVTVGVKG GPPSVFTEISWEVLEMVTGGVG
29284	59652	A	29459	1	330	
29285	59653	A	29460	140	214	
29286	59654	C	29461	181	381	
29287	59655	A	29462	427	957	
29288	59656	A	29463	3	241	WLRERAPEGSPETKGS/PPPPP RSVLHLSA/SSPLRPPEGL*TC RGSPSADSPRRGKHGGKTHLV SWLSQQKIPMAR
29289	59657	A	29464	122	473	
29290	59658	A	29465	1	771	
29291	59659	B	29466	1	1017	
29292	59660	B	29467	1	2568	
29293	59661	A	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I SQ*PQORYECRDNQQLDQL/V/ EQFIQTLEKAITQHRQQLNQWT QKVDIARRR
29294	59662	A	29469	1343	1714	
29295	59663	A	29470	321	2645	

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29296	59664	A	29471	611	1215	RWCVWSLFLQML/EMCPFELPS GGFVVSLSGSKVLQFTFTVNVTA HKGSVDPKRVKLTALVSVTA LKAACLELFLPPGGFVVFAGFR SEAADLCAEGASSGLGQPREGL PRCSGGLKGSSSAARMGAEAK GAPRASQGCGRHHAVTSHRS DMGEEEGESQRYLSCPQSPCP NLLQEDASKVIVFAESGINPDSV LDLIMLH
29297	59665	A	29472	335	453	KYIWNVNLQHSVSMLL*FITS*L SGMDSLFPAAHCV
29298	59666	A	29473	1	1041	
29299	59667	A	29474	3	874	TEGQKNLIVEVTSNDVVRFP WTIDNKYYSSADINLCVVPNKFL VTAIEIAESVQAFVVFSTQKS GLDSVSSWLPLAKAWLPEVMI LVCDRVSEGINRQKAQEWCI KHGFELVELSPEELPEEDDDFPE STGVKRIQALNANVWSNVVM KNDRNQGSLLNSLTGTNHSIG SADPCHPEQPHLPAADSTESLS DHRGGASNTTDAQVDSIVDPM LDLDIQLASLTTGGGDVENFE RLFSLKEMRDKAATLPHEQR KVHAEKVAKAFWMAIGGDRD EIEGLSSDEEH
29300	59668	A	29475	1	1773	
29301	59669	A	29476	1	1023	
29302	59670	A	29477	2	616	
29303	59671	A	29478	1	972	
29304	59672	A	29479	1	339	
29305	59673	A	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG EGTYGTVFKAKNRETHEIVALK RVRLDDDDGVPSSALREICLL KELKHKNIVRCAGGGCSLPVW PLGGGGG*HWTSVRRRTCLAEFF FCPLRLHDVLHSDKLLTVFEFC DQVKGGVWRTVALGR
29306	59674	A	29481	1	843	
29307	59675	A	29482	1	873	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 95/40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
29308	59676	A	29483	13	945	NRGPAGVPAAMQKYEKLE KIGEGTYGTVFAKKNRETHEIV ALKRVRLDDDEGVPSALREI CLLKLKHKHIVRLHDVLSHSDK KLTLVFEFCQDLKKYFDSCNG DLDPHIVKSLFLQLKGLGFCH SRNVLRDLLEAPATWLNREW GSWKLGVDFGPGVRAFVGFPV RCYSAEV/VSHLWYRSPDV/LF GAKLYSTIDMWSAGCIFAELA NAGRPLFPNGDVDDQLKRFRL LGTPTEEQRPSTMTKLPDYKPP MYPATTSLVNVVPKLNATGRD LLQNLKCNPVQRISAEELQH PYFDFCFPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE
29310	59678	A	29485	3	1225	
29311	59679	A	29486	1	864	
29312	59680	A	29487	1	1413	MVNPVFFDITVDGEPLGRISFEL FADKVPKTTENFRALSTGQKGF GCKSSCFHRIIPGFMY/QGGDFT RHNGTGGKSIHGEKFDDENFIL KHTGPGTSLMAIAGPNTKGSGL FIYTAKSEWLDGKHVVFGLSR GDSLKEPTSIASSRHPSYRSEP SLEPESFRSPTFGKSFHFDPLSSG SRSSSLKSAQGTGFELGQLQSIR SEGTTSTSYKSLANQTRNGSL YDSSLTPSDSPDFESVQAGPEPD PPLGYTSPFLSARLAQQREAE HPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLPG REEEPGLGDSGIQSTPGSGHAPR TSSSSDDSKRSPGLKTPPLGRPAV PRFGKPDGLRGRGVGSPGPGPT APYLGRSMSYSSQKAQPGVSET EEVALQPLLTTPKDEVQLKTTY KSNQGPKSLGSASPGPGQPLSS PTRGGVKKVSGVGGTTYEISV
29313	59681	A	29488	1	3126	
29314	59682	B	29489	46	114	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29315	59683	A	29490	1	704	AALLALGPRNPWTLWTPLT PNYPDRQPWTDKHPDLLTCGRCL QTFPLEAITAFMDHKLGCQLF RGPSRGQGSEREELKALSCLRC GKQFTVAWKLLRHAQWDHGL SIYQTEQRPRPRSWAWPRWL QPCRQWWGQQLRPRAPV/HSG SGLTRRSPTCPVCKKTLSSFSNL KVHMRSHTERPYACDQCPYA CAQSSKLNRRKKTHRQVPQSP LMADTSQEQASAAPPEAVHA
29316	59684	A	29491	3	1605	
29317	59685	A	29492	1	453	
29318	59686	A	29493	2	128	
29319	59687	A	29494	1	543	
29320	59688	A	29495	39	1092	
29321	59689	A	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/ TLRPKAL*LTFSQIFSA*RLKTD TARSPRKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
29322	59690	A	29497	1	281	VSDHAGTPALVLHP*RVQVLF* GRGKYPTSPSPPLAELATSAR NLTRPRNACSPGFLPSRVPSVR DPTGNRTVQLTWQPLPEPLEL WPKAL
29323	59691	A	29498	1	542	MRAPPKSGQLQHCPRSGALRS GDLPEWEINPLSSCSLLHEKDP MTSGPQTNPQKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAIPYFRTPSY LCAPIPVYRTPTSYLCALTPPL FWRHIRTSKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPGQGMPPAAQ
29324	59692	A	29499	1	1044	
29325	59693	A	29500	596	833	LLLDLPAED*CCLIASEAP*TITD AEL*VTLTVEGKSVPLINTEAT HSTLPSFQGPVSLASITVVGIDG QASKPLKNE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSLPFRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCPTPTPYFHDPTPFPLFW KELATCAGNLATGTRNAGSPG FLLSRVPSVWDPTENRTVQLT WQPLPEPLELWPKA/HLTDSFP DLGLAA\ED*HCTIASEAP*TI/ TDAELWVTL\VEGKPPFPLINT EATHSTLPFFQ\GPVSLASITVV GIDG\QA\SKPLKTPQ\WCQH* TIRRFKHSFLVIP\TCQVPLLG\E DTLTKLASLTIPGLQLYLIALA LPNPKPPLRPPLVSPDLNPQV*D IGVEWGKGD
29327	59695	A	29502	6958	7935	
29328	59696	A	29503	1	486	
29329	59697	A	29504	1	492	
29330	59698	A	29505	2	502	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLLPAAMVNPTMFFH IAVDGEPLGCVSEVRGLESKK *LL*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFYKGCSCFH RIIPGFMCQGGDFTRHNGTGK TSKKITADCGQLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFFDIAVDGEP LGRVSEFVRGLDTKK*LL*SIK LC*QIG\LFADKVPKPAENFR/A L*SIEEKGFGL*GVPCFHRMIPGF YVSRGGDFTPP*MAPGGQVHL MGKKFER*RTSSLKHTGVGHL VPWANA WTQTMGMSQFFICTA \KT\EWLDGKHVVVLAKVKER HEILWEAMERFWVPGNKTS KKIISIADCGQLLISFDLCFYLNH QDHSLLCSPRESTPLPHLLAGS
29332	59700	A	29507	1	380	LCSCP RRRLGREGAGEPTSP VTQYLQPRSP ECKMFACAKL ACTPSLIRAGSRVAYRPISASVL SRPEASRTG/EGAA TVGVAGSG AGIGTVFGSLIIGYARNPSLKQQ LFSYAILGFALSEAMG
29333	59701	A	29508	76	385	EEPTSPVTQYLQPRSP ECKML ACAKLACTPSLIRAGSRVAYTP TSASVLSRPEASRTGEGSTAFN GAQNGALH\I\QRELHTSAIRRD IDTWCKFIGCSAATE
29334	59702	A	29509	2	230	
29335	59703	A	29510	242	427	SAPDLTCNSKTWKNGR\ICFHP ASLVSLY*QPQLASWTMKKQD ENTQEGKSWDSFSDVIHI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29336	59704	A	29511	1	1497	
29337	59705	A	29512	199	766	EEPTSSCHPNISSRAVP EECKMF ACAKLAMRPPSLIRAGSRVAY RPSVASVVISTQRLSRTGEGST GI*MGPPQNGVSIQLIPKGSFQTS CNQAGGHLITGCQIYLGAGCLQ Q*GVGWFLVAGIGNSLLGKPY LG YGQKTLSPESQQLVPP* CYP GDFALALKLKMAGLFC/LMVA FLILFADVTEITA
29338	59706	A	29513	427	840	
29339	59707	A	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ* DGTLLC/R CGS*GLPTFKKSTCGKCGYP AK RKRKYNWSAKAKRR/NTFGT G RMRHLKIVYRRFRHGFREGTTP KPKRAVAASSSS
29341	59709	A	29516	1	668	
29342	59710	A	29517	649	992	
29343	59711	A	29518	1	2994	
29344	59712	A	29519	3	486	
29345	59713	A	29520	2	898	NSRVDDFVCPSSRRSKRD LIEFS CRILFPLPSLPPRISFIHPSPTLAR VRIGGAVRRPHQSHSISSSFGA EPSAPGGGGSPGSLPRPWGPKS CSSSLCGARS*FFWRDVKNTGL VFG/TTLMLLSLGSFSVSSVVV S/YLILGFSSSVHHQLSGI*QSSV PSCNRKFRKKGHFPQKPNWNV DITLSSKSF SINNMNAAMVHIN RALKLIIRLFLVEDLVDSKLAV FMWLMTYVGA VFNIGITLLILAE LLIFSVPVIEKYKTQIDHYVGI ARDQTSIVEIKIQA LKPGIAKK KAE
29346	59714	A	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGFFFTQVANIIS VAVNLVFCIRFLENTGVIGTI* R RCPIPFSAW
29348	59716	A	29523	1	4368	MLFSYLEKYFYVADEL SHC VEP EPSQVPGSSRD RQQ GKPPPLP ALKAKTSSRSGPYATEIKKSTD DSIFKVLDFWNRSSYSDDNK/LI PPTSPRNRVQKRN/PKSQVAV DLVTD DTTLRENGSKTLSPSKIE LKPVRSDDSPQAEGDMLVSESC QDNNVNIKS FKMNL SKQGT PK EGPGILQPFESYGTSPSQGKNM DYSQDSKSPGKGNGASPSNSNY SYSVLKESDAENQVPCNTNNIG NLGEEEPKFHAI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
29349	59717	A	29524	33	3339	TDQAKVDNQPEKLVRSAEDVS TVPTQPDNPFSPDKLKRMSKS VPAFLQDESDRETDTAESSY QLSRHKSPSSLTNLSSSGMTS LSSVSGSVMSVYSGDFGNLEVK GNIQFAIEYVESLKELVHFGAP VEGLNSSGWKKTGVIPY*KG/Y LLPNKGQMGKKTLVVKKTIN PVYNEILRYKIEQIL*TKLNL SIWHRDTFKRNSFLGEVLDLE TWDWDNKQNKQLRWYPLKRR AKALQRFQLKAMGNS
29350	59718	A	29525	946	1183	
29351	59719	A	29526	2048	3359	
29352	59720	B	29527	1	300	
29353	59721	A	29528	1	1495	
29354	59722	A	29529	1	2769	
29355	59723	A	29530	450	3061	
29356	59724	A	29531	421	1464	
29357	59725	A	29532	238	930	RLSLVSSHCGTILSSEVVCAPPT AYIDFARQKLDPKIAVAAQNCY KVTNVAFTGEISPGMIKDCG/AT WVVLGHSEKRRHVFGESEDLIGQ KVAHALAEGLRE*FACIGVEKL DERIEAGIH*GRLFFEQTCKVIAD NVKDWKSVVLAAYEPLLAIGT CKTSTPQQAQVEHEKLARGWLK SNVSDAVAQSTRIHYGGSVTGA TCKELASQPDVDGFLVGGASL KPEFV.DIINAKQ
29358	59726	A	29533	1	929	
29359	59727	A	29534	3	623	
29360	59728	A	29535	3	202	
29361	59729	A	29536	1	1046	
29362	59730	A	29537	1	1320	
29363	59731	A	29538	1	1052	
29364	59732	A	29539	922	1245	NRCLGNSFKCLCILQVGRAHA FLLCSDFMPEAVCSSIHSFIPV TKTQGAAPHTRAHSLTPDPKPS CCCCCPRPGEDPGHMCVVWP WQPSVIYAKYWTYEHQAQW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS GHYALQEAQETSQSRESQA
29366	59734	A	29541	1364	1916	
29367	59735	A	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ PWAMIIDVFSRYSVSGSEGSTSDP *PKGELKVLMDKELPRLSLQS GKDKDAVDKLLKDPGRPMGD AQGGTFSEVHPCSVAAITSA/C HKYFEKAGLKLMPWEMFTDF LGQSIGSQGFPMFCLGIYFP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29368	59736	A	29544	175	355	FSQQLLGQAD**SFLLAGCSRLLTAVSRPKRPGEAGITPRVRCLLSNMKDILVASKFWQL
29369	59737	A	29545	482	1196	
29370	59738	A	29546	196	818	
29371	59739	A	29547	170	370	
29372	59740	B	29548	147	257	
29373	59741	A	29549	1	1278	
29374	59742	A	29550	2	152	
29375	59743	A	29551	2	187	
29376	59744	A	29553	1	915	
29377	59745	A	29554	62	430	RQQDELALIAETLKCVDH*LSDLVLPARGCA*HRELCIHDLLKGNPLRRNLAG*QTERMQLQVESQSIPEEILGLQPQLGPMGGLWNVRFLLIPTVLWGFHCSQERAFPRKLQVKSFPVAQG
29378	59746	A	29555	149	381	
29379	59747	A	29556	1	656	
29380	59748	B	29557	146	1320	
29381	59749	A	29558	629	1417	WCASHWWSGHAARHA*ASHPLHGLLCSPLPEEHHPLLHGAQS HRPKPG*GM*AHGTLAGSSTCSPAQGL*IHQSAPCV*LKVCECTNRHSVSSCSDDEDVCISLCLGQ*GP/ECI*CRIFLGPFRNLIEGAPHL/CRSAMLNPLQEGAREQASARSGWLLRLLTQEQLLRCRACIQTRDREGKTRHRKGTPEIGKGRFVWKKSLKILILFNCLRYWNAYMEIWWPALTGIPNVTVNYATSSSKDSRTDGRVDLLMAVTDGM
29382	59750	A	29559	318	608	ISQARRAAPWGPVQPEPSR*APPASGHPVPSTTQRLRSAGARRGTGGQLHLQPRCGDPLGETSWAPESRRSAASLLKPARPRAHWEEQITPDALL
29383	59751	A	29560	88	564	SCLPVLRRALFLSPWVVDGTGRRGAAGGGRWGGSGRTGAHGVGRLRHGGLQVPSALQEGS*GSVRNRAQPGGLALLGDPVHPLQPLARVLSPLPG/DQQGWPAAPSVGPTKPTTRNSSWPPSAAHSPGSCSLSLHTSLESCRCPSINTSLHKHA
29384	59752	A	29561	3	339	RYKDSRPHQTQEPSWLHLVDPAPRLQVELPASPALCARIPQPLGWHGTGRRRGQGAALVGEARAGLPSLPSFFFSLLSFLSFFLPSFPLFFSLFFPFCPVNCGEQCPGKGM

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29385	59753	A	29562	327	890	VMRIQVLLYYLRFADQGTGFH LVLCLRHTAGVQ*SWDS*SGLT PELV/HLDGSHV/LAASPRGSPG/ SPK*MGADQRSESSPGPGGG PRAEGPHHIQEAPRSA*AQGAG AEAAARLGAGQASGCQSTRRPA GSRREPGVSLDGGHRAVVGIQF QAPSRRAA WGHPLHDA PGRRLL MSRQLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGQWLRKVVVWPQQCRPTG AVLDFSPGCSCLPAGQSGGPAA RHA*ASHPLHGLLCGPSI.PDEH HPLLHGAQSQRPPKG*GMRAH SAGLAGSSTCSPGAGSTR*SQL GS*VW*GRGESLCL
29387	59755	A	29564	1	2715	
29388	59756	A	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ KLLHFLYSLQKGISPNAIPPHSP HPTTAPVYSSQCERRRRQVISAF PT/GD*SLHSN*E*QGGVEGEAP AGTWAVRGA*GPAGVPGGRGL GGLRTRSSWPALLAPGRQSGSP AARH/GLSLPQPPWAPVQPEPP* GAPPPAPRRPVPSATQGLRSAS ARRRTGRQLHLQPPCGIHLVKP AGLLSLVGTWRVFM
29389	59757	A	29566	1	470	MGQPLLLVRDSSGGLQLWQKV KGEPVQQHERRIIPAREEKVK RSPAGPPSPGGLDSSRHKIPSHE QA/SGVQPACKTTHQPRGIWCS PSLPDEKCPLLHSAQSHRSPKG* GVRAHGVGLAGSSTCSPSAGSN G*SQLGS*V*NKGR*YIPRTGRC
29390	59758	A	29567	777	1063	QLPPPSVFPTTPKTELVLGTFPH GQPHRGGHESSDSAGGHLPL/R ALRSGWDPSPPSVCATPTSSGL SSTPQLPLHQRRTSSSTASWSPG WGMGSC

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29391	59759	A	29568	195	1899	GSASGVVRSRRWARGLAGFRS EAADLHSECYSS*KQCGPKD*A EARFIAKSEGTKLPQCGRGPH*I QRFSTSPDSDGAQLASPSGSRTR AAGGAACQSWCRAP/STPQPLG GRWDWAPWSRGWRSSGTSGR TGAHGAGGR/PQAWRAAGPQP CPAGRQLRPETLKQNIILSLIQCI GASLVPTGTAELEPSPSQLRGRT TDAAQAIAKNEFARVQKRNLCR RGPICFEGDALS WFFEKINKIDR RLARRIKKKREKNQIEAIKNDK GDITTDPTETIQTIREYYKHLYA NKLLENLEEMDKFLDPTYLPRIS QEEVESLNRPTGSEIEAIIINSLP TKKSPAPDGFATAEFYQRYKEKL IVLEVLAARIRQEKKEIGIQLGK EELKLSLFADDMIVYLENPIVSA QNLLKLISNFSK VSGYKINVOQK SQAFLYSNNRQTESQIMSELPFT IASKRKLYLGQLTRDVKDLFKE NYKPLLNEVKEDTNKWKNI PC SWIGRINIVKMAILPKIEKQTWN NSQTLQCQPFCESDVCTSTLQIQ ERFEVAPLHKALSSIEITIDKT DPSPAIEELTV
29392	59760	A	29569	77	640	
29393	59761	A	29570	384	746	APWSRGWCSSGRLGLHRSPWS GWEAQAWRAAGPEPRPAGRQL GAMSCKVETGT*DSEQRHFRFG ESWGHWPWAGAQPTGPVLSGIL NVLSFSVLALPRPTGWPRPCS AASPSRCPAQSHQH
29394	59762	A	29571	189	545	GLSCLPAGQSGGPAARHV*ASH PLHGLPCGPSLPNEHHPHLLHGA QSHRPPKG*GMQAHDAGLAGS STCSPGAGSTR*SQLGS*VCCGTG RLVGTQQLRPESG*VSQSPRL WAAAEAGSC
29395	59763	A	29572	87	374	AYSSQLGESRRYSLDQCLAK*I CEGRTCIFEPCNCSSLYVRSNG GNHSHSTTTFKYNGSNWIPRW QGPSGSTQPSKARRPVAFSQGN CAMEKGN
29396	59764	A	29573	1	2453	
29397	59765	B	29574	182	1356	
29398	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS LGLSCLPVEQSGGPAARHA*AS HPLHGLLCGRSLPDEHRPLLHG AQSHRPPKG*GMRAHGAGLAG SSTCSPGAGSTRNREN

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29399	59767	A	29576	142	442	PKG VGRALAAFPQDRAPGPAA RHA*ASHPLHELLCGQSLPDKR HPLLQGAQSHRPPKG*GVQAQ GTGTGRQLHLQPWCGIHWVKP AGLLSSLGPRCFYKL
29400	59768	B	29577	1	2464	
29401	59769	A	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL SPWVVDGTGCRGAGGGAHRG GSGRTGAHGVGGR/PQAWQAA GPEPCPMGRQVRPGEKSSAVPV GQPGWGTQYTLRSHWLGC
29402	59770	B	29579	1	2598	
29403	59771	A	29580	1	2028	
29404	59772	A	29581	5917	6355	QEAQPEESANDAQGDGPPGGK PQPQPEERSSCAQGVGPPGGQQ ESQDEERSSDAPEDGPPGGQQK PQPPEERSSDAPEHDPGGQQQP QPEERSSDAPEHDPGGQQQPQ SEERSSNDAPGDGPPGGQQQP*P EERSSGAPGHSSPDV
29405	59773	A	29586	875	2090	
29406	59774	A	29587	228	505	MLGRKPNHTSASRNTRLRHCSR ARAQVKRMQRQREEREAK/R QPGTASGTSGIAERDSGKCSRK RGVQKVPG**NTRQSKLRPREQ CTTADP
29407	59775	A	29588	188	592	AAPPRSPSYRMIRKTR*MLGR/E AEPHVCQEHQVEALQHGGGP GETDATAAERR/RGRQRRQPGT ASGTSGIAERDSGKCSRKRGVQ KVPG**NTRQSKLRPREQCTTA DP*TLSTFPPEGRGTELEPGFDSG ASVLMRGCRALASASSPQGP GPQEM*ATRNWGRRQ*GRHC KLPLVLTITGLQGDVVEGVHVG ASQEPLIQNDOEVDVAWQKA EPHVQEQEIHQVEALQHGGGP ETDATAAERRAGGKDASLVQH LVPVALLSVTQGSVPEKEEFKK SLVNEILGKVNYDQGNVVPQ TLEHCPFPKGEARSWSLASTP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRQPQTASG TSGIAERDSGKWSRKKREFKKS LVNEILGKVNYDQGNVNPQQT PSHHPNLEHCPFPKGEAGAGA WLRRLRLGSGYEGLPGCALCFFF PSRVLGLRRCEQGEIAGQQQGR DTQHGGQ/RSAGEGRGRPG*GPG RTGPAAQLPQSLRTTRRSRPW GRRQ*GRGR*PPQGLMRC*RRP HHTGWSFPQNEKRQPGRSFQQH KSH*RE/RR/RARPVGQVQVAK RSQQFDDECEGDVREQHSSRRD RVAVKS
29409	59777	A	29590	2	394	
29410	59778	A	29591	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESPSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
29411	59779	A	29592	1	561	
29412	59780	A	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W TALWEMLYAEANPFSTIRILF QLEQPALGTSQYKILCSST
29413	59781	A	29594	2	704	WRGGSGSGGWESGRRGFFVAL PERSGVCQVVSIMFSNMFDP IPRVFQNRFTQYRCFSVSMIA GPNDRIMPSPALDQLSRLNITY PMLFKLTNKNSDRMTHCGVLE FVADEGICYLPHWMMQNLLLE EGGLVQVESVNLQVATYSKFQ PQSPDFLDITNPKAVYLFQISGV LLDKGECAGECVCRLENALRN FACLTGDIIVAINYNEKIYELRV METKPKDAVSIIECDMN
29414	59782	A	29595	1	1680	
29415	59783	A	29596	1	2220	

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29416	59784	A	29597	2	1114	SGRRGFFVALPERSGVCCVVSIMFSFNMFDPHPVFNQNRFTQYRCFSVSMALWPNDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFKLTNKNSDRMTHCGVLEFVADGICYLPHWMMQNLLEEGGLVQVESVNLQVATYFQELSSCYLPHWLMQNLLEEGGLVQVESVQPFKWATYISNFPQSPDFLDITNPKAVLENALRNFACTLTGDDVIAINYNEKIYELRVMETKPAKPVSIHECDMNVDFAVPLGYKEPERQVQHEESTEAGEADHSGYAGELGFRFSGSGNRLDGKKGKGVSPSPKPGDIKRGIPNYEFKLKGITFIRNSRPLVKKVEED EAGGRFVAFSGEGQLRKKGR
29417	59785	A	29598	15	569	
29418	59786	A	29599	30	525	YCLHHFFQVSLVFAWCSEMHGNRQLWEIRTEGMRRTPLGSWTAKSPIGR/SLRSARVPRTVAHSQRAKGSHSLWVLRPQKRCAGKSPPPSRLARSPRCEPLVALARQPLCVRRAGPEERARAQRPRPRVPLLSQPGRALLLLLRS SFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	
29420	59788	A	29601	758	1076	LPMNRPPRWITGLAPIELLLLELQQKENMALGSRTHHGSSPNSGSAFCQMACCSSLPAL*SGRC SQP*WLWMSPLSRFISINSTAS SSSIGNAIRRRSRPGP
29421	59789	A	29602	632	835	
29422	59790	A	29603	428	1214	FIATVLPWHRSPQWYYPWVRGPVTA/LVRKVPVAVAGERSLWSVVGILWKPLGLALQGVGFVIGTFVSLYFASKGWAMAGFTLTAFGGAFVVMRVFMFGWMPDRFGGVKVAIVSLLVETVGLLLLWQAPGAWVALAGAALTGAGCSLIFPALGVEVVKRVPSQVRGTALGGYAAFDQIALGVSGPLAGMLATTFGYSSVFLAGISA VLGIVTILSFRRGQETAHQPDQQRAAAYDLQRSNRRVLPASPASACRCSDAHSR
29423	59791	A	29604	1	825	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29424	59792	A	29605	242	945	NGCIVRGKTSGSTFICVAMSVA ASTVRR*CWLPGRKAAAWRTC WAPMT*AVMC/WSRLMYGAR LSLLVGCLVVVLSLIMGVILGLI AGYFGGLVDNIIMRVVDIMLAL PSLALLVLVAIFGPSIGNAALA LTFAGLPHYVRLTRAAVLNCL APLIVQASLGFSNAILDMAALG FLMGGAQPPTPEWGTMLSDVL QFAQSAWVVVTFPGLAILLTV LAFNLMGDGLRDALDPKLGKQ
29425	59793	A	29606	1	2433	
29426	59794	A	29607	1	1383	
29427	59795	A	29608	1	218	
29428	59796	A	29609	1055	1873	
29429	59797	A	29610	3	823	
29430	59798	A	29611	183	1163	
29431	59799	A	29612	4375	5125	
29432	59800	A	29613	1800	2031	
29433	59801	A	29614	2	848	
29434	59802	A	29615	886	949	
29435	59803	A	29616	123	315	
29436	59804	A	29617	34	343	HLCVSRGVYAADPYHHALAPA PTYGVGAMNAPAPLTDKTRTS HADDVGLVLSLQASIRGGY NRFAPY*MTKP*KPSNVGRKEA FRGLSIAIHAVVHHFSNS
29437	59805	A	29618	1	305	AAAYRG AHLRGRGR TVYNTFR AAAPPPPIPAYGGVVYQDGFY ADIYGVMLHTATPSLPLPLPLP TVTVTDEFMTFSPLSPLTCSSPH LRRWCEHCFCTFD
29438	59806	A	29619	1	2115	
29439	59807	A	29620	1	273	FFSRVVPDSDYQAQA/MVDIVT ALGWNYVLT LASEGNYGESGV EAFQISREIGYPSLFGIQGCLHE CFAILCQVVYQFLLMLQLSDAQ TVY
29440	59808	A	29621	1	405	
29441	59809	A	29622	1	582	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29442	59810	A	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS ICYSHGRDLAPARPAQPPQPRD QPQVRPLCSPHAAAAAAL TWSGPPAGFLTAPSAGSRVRL AARQKKAAPRKASAEPRDKKP LAPKLQNALLVGKESPRFIPL SVFFSKTFQRTARILKRSADRL PWVTSRTPCGGIRTCPAEMTRY LRFANLTGGISEVSGFRDEGIN FGSWIAIPPVKMCVCEGKRAS CPCFFLLTAKFYWLTMMQRTH SQEYAHISRVDGD
29443	59811	A	29624	1	2740	
29444	59812	A	29625	1	1614	
29445	59813	A	29626	88	540	
29446	59814	A	29627	2	577	
29447	59815	A	29628	1	2169	
29448	59816	A	29629	1	1619	
29449	59817	A	29630	674	867	LDGDGIESINSLGQYGHFDIDS SYP*AWNENLVPFVCILFYFVE QWFVALLEDVLHVPCKLDS
29450	59818	A	29631	746	1985	
29451	59819	A	29632	1	2211	
29452	59820	A	29633	139	247	KTSAAHEKPKWRKERNARG* KRKRRLQMSQVNR
29453	59821	A	29634	335	556	
29454	59822	A	29635	1	586	
29455	59823	A	29636	908	1260	
29456	59824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA LSPDEFISPVCLARLVWRFC FAQKAR*SPAKYGILGELTTGS KLVLKANGLMEASTIAAILGVS AGGVLA YWHVLVA WPHAHWP TVSRQQQLMASTLPFTSPLAQ IFPWRITQRTMRMPFVIDARD ALLQGVFAAVNPSAHLNDSRH RRINKNVIEPGISQRPQHLDR AHPFGIHHQLNAFTGRQFHQR QLLYLRQTFFVVDIDHHHPRLY AAVNGVIDSANAHRTCTRQQC NIAARFDAHAMLINILRGVIIGM ISTNNAHRLCQRRRSKIRSDT GNTQPKLMQI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH CWTAVACHQCEDAPCANVCP VDAISREHGHIHVEQTRCIGKKS CMLACPFGAMEVVSSRKKARA IKCDLCSWHRETGPACVEACPTK ALQCMDVEKVQRHRPRLNFLR LWYVVHAHTLMRMRPRFIQPW EEVVPRIHQHAACFQALIELLG RNGQILKP
29458	59826	A	29639	391	812	HSALCSCRMRRERLIRPTKTCK FNRLQRLCRPKRSASGNFAVV IRLERVSLAPFFYGVLKCL MPKRQCNEADHHQTHTCAGQ KKMATHPLPGENKFIIGEDREY RWALMFPNENAPVCWVGHVR *KSPLHQHIDRA
29459	59827	A	29640	589	1075	
29460	59828	A	29641	1	435	
29461	59829	A	29642	9	661	
29462	59830	A	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	A	29646	114	851	CDHRNIVIRSAENISANFSHTGS V*GWMFTVP*SPSGRVVF*FCH L*ATCGN*LN*THSLSQGQRAF CILGFLPWHSRRIRSHVGLENEC KVLLSGRSSQMGEP*GR*FSP* VGPLGGRALLQLPQPNV/YVL PVSGLLVPAGE/CPLNV*PLVCS SANVLLSTSSCFCLCLARVSGF YRHRMGA/SGGFL/M*V*RKGS SFNFLHMA/ASSWDSYSGHHFF *AGADYFFASSVSSLPLVLLHSL HSFF
29465	59833	A	29647	1	1422	
29466	59834	A	29648	1	768	
29467	59835	A	29649	1	885	

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29468	59836	A	29650	1	1253	MVSVTALKAAFLFIPPSGLV VSLASGVKLQTFVSVTAHKG SVDPKSDQHGLVSLASGVKL QTFARRAEFPASQQQREVPRHD GGNHADRFTIIDHRLMATGG RHFAIHFDVDRFGVPANGARRAG NIITQTVTNRFAGVESFQQCQLF GIYAVCERQGAIEIPGYARLFL ATFFIYTSSFPPPLPWLRLPRN ITPAVVRTAKQVTAKYVIVA GNAYLGDVPELAKRSMPCG TQVITTERLSDELARSLIPKNYC VEDCNLYLDYYRLTADNRLLY GGGVVYGARDPDDVERLVVPK LLKTFPQLKGKIDYRWGTNL QLTLSRMPQFGRQDTNIYYMQ GYSGHGVTGGSSRVGLMAGSQ ISRVS/CIN*YHRFNLHWRYV ADAISADGAFTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRTDISLYQHTAEQKHPYCW YYPADSADI SVNKHRRNATQ LHVSCSFLLSDQRFHHEAVPR RVVLFTFNTCDKYIADIRSR NGLGLYAFKQRNSHFVNAQ RHRHSACLR
29470	59838	A	29652	1164	1273	
29471	59839	A	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT EEALDQSNADLITLLADWFKDL GFNVVQPVPGTRNKFNMLAT RRHEGRYITCMQPLPIAEQE PEMTVRYIYSSADLTAEKFATA IRNHWHVENKLHWRLDVVMN EDDCKIRRGNAELFSGIRHIAI NILTNDKVFKAGLRQGWEDIED FGETHLDFLKQYQDFENGIPVH DTIARVVSICSPAKFHECFINW MRDCHSSDDKDVIADGKTLRH SYDKST/RRRGAIHVNNAFSTM HSLVIGQIKTDEKSNEITAPELL NMLDIKGIITTDAMGCQKDIA EKIQKQGGDYLFVAVGTQGRLL NKAFFEEKFPLKELNNPEHDSYA ISEKSHGREEIRLHIVCDVPDELI DFTFEWKGLM
29472	59840	A	29654	2	1587	
29473	59841	A	29655	236	666	
29474	59842	A	29656	1	1953	
29475	59843	A	29657	2202	2333	

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29476	59844	A	29658	1	1126	MHEVTLEDSPSSAQILITVITGHG EITLKRSSRRQNDIRMYCRRRP EAFRDHHQLRFLPGTDQAIGL MMSKVGTA RPPDKTNIREMSV HTVVLI CATRVFCFNNAGNR DFIHRIAATRQAALHGREGHRT PRGVTITGKMVRKTKTAAGWE HESGFYLDGVVKLNRFKSNVA GKMSSGGAANGSYHSNGLGGH IETGMRFTDGNWNLTPTASLTG FTADNPEYHLSNGMKS SVDT RSIYREL GATLSYNMRLGNGM EVEPWLKAAVRKEFVDDNRVK VNSDGNFVNYLSGRRGIYQAG KDLDRFKNLVLVHAARYAADL SYLPLMQELEKRYEGKLRIGTV VSRETAAGSLTGGRYH* LKVG NWKARLACR
29477	59845	A	29659	1	1989	
29478	59846	A	29660	3	159	YKELNLADSSLSEEALIQAMVD IPKLMKRPKV VANGKARIGRPP EQVL IEIVG
29479	59847	A	29661	360	744	
29480	59848	A	29662	1	996	
29481	59849	A	29663	441	446	ICRQYPSPDDRTASGAGGGDHQ QYGAGLRQTFCLCQRLSARTC* RLSASVCAT
29482	59850	B	29664	1	1608	
29483	59851	A	29665	1	2568	
29484	59852	A	29666	116	283	
29485	59853	A	29667	207	1270	
29486	59854	A	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
29488	59856	A	29670	1	1167	MPWLSTGAAALITALAVVELN DDDDHHHRNNSPLPTPPDDES DDTPVPPTPGGDEIIPDDDDTP TPPKPVSFNNDVILDKTEKTLTI RDSVFTYTENADGTISLQDSNG RKATINLWQIDEANNTVALEG GNTSACRQALKIPKGSDDYTVT WKGGHFTFYRRWRCKVHKVV FEGSPPTICRYVLNRKNSWHV AHIFRRHAKPEEQ/CSHLFPYPF HHDLDEVLNDPDKLVVVCCT HADSHFEYAKRALEAGKNVLV EKFPPTLAQAKELFALAKSKG LTVTPYQNRFRDSCFLTAKKAI ESGKLGIVEVESHFYDYYRPA ETKPGLPQDGAFFYGLGALFTNQ QGFFKSSLLSIFADSSSSVAGRS PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	A	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	A	29674	282	660	GPSSEPSWAYAPGKAGDPHHS AEWARNSTPSKDQA*RRPHTVIC VTAYQGVLLVGQSPNAELSA RAKQIAMGVGDGANEVYNEIRQ GQPIGLGEASNDTWITTKVRSQ LLTSDLVKSSNVKVTEN
29493	59861	A	29675	720	4525	
29494	59862	A	29676	218	990	
29495	59863	A	29677	54	723	
29496	59864	A	29678	1	2229	
29497	59865	A	29679	2	235	
29498	59866	A	29680	279	1275	
29499	59867	A	29681	692	1052	
29500	59868	A	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD CWVDDARLVLANAQMVVRKG GEVLTTRATSARRENG/GKKY SWQARGLESLSQPVERLSP
29502	59870	A	29684	1	1941	
29503	59871	B	29685	1	4107	
29504	59872	A	29686	840	1006	CHESHRTDGGAVFRVYPGGG PRRECWFGSSSLDEATPGWLLQ/ LYERDRH*PASTG

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29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRLKRLLSRK TRMP/GFTNPRYGAGAAATNDP EVFSWAATQVVTAMEATHKLG GENYVLWGGREGYETLLNTDL RQEREQLGRFMQMVVEHKHKI GFQGTLLIEPKPQEPKHKYDY DAATVYGLKQFGLKEIKLNI EANHATLAGHSFHIEIATAIAL GLFGSDANRGAQLGWDTD QFPNSVEENALVMEILKAGGF TTGGLNFDKVRRTSDKYDL FYGHIGAMDTMALALNIAARM IEDWQLDKRIVQR
29506	59874	C	29688	1	2130	
29507	59875	A	29689	238	1879	
29508	59876	A	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR KSVRTQVLSAADVRAKLFTLK VQDPKIDRANPTMVNMRWMM SA
29509	59877	A	29691	596	723	MCASAP*WCELPAGVVRPPAST TADYFPLFTLVHGGCAHGRF
29510	59878	B	29692	1	441	
29511	59879	A	29693	1	1422	
29512	59880	A	29694	1	2856	
29513	59881	A	29695	2	367	QKAGAVQVLLSLWSSLSAAAA GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS GSLDRPSALHSGTILSGKITSDIC CPHF*SPGRPCSKQHWAEMLV HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLEITSPAIIFSPTLHSPAHH HQYRKALHGRFPARSRDPPALA PGWRSARRER*SSPARAAARW CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE SYSFTDSV
29516	59884	A	29698	279	732	PPGATLPTVARGTPQMKGESS PAKSLAPPLCEQMGGQEDGHWG AGWGLAQVLLIALDGLLDAQQ HGGEPLGPAGRWSPRSPTRCS CPHSAPRGPLAIFSSTCIPGNQR KLGTAPHTFGQPAWR*ACRCRS GRGPP*RSSLWRCTEEGAVH
29517	59885	A	29699	353	2776	
29518	59886	A	29700	158	605	PERSGLQEAGGSGRGWGKRSL PPAETAGLSGYMCFRAWLSLRS WDESDGHWGAGWGLAQVLLI ALGWSS*CASNGWLSHWFQPG R*SRIPFTDSV*LVHILLPVGPL AIFFINLAFPIRESWEQLLILLE KPVGLEACPCCKSGKGRP

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29519	59887	A	29701	1	753	MLALDQREAMRMIFPAVAGAP APALSPYAS/ARILVDQQFCYRQ VVEQNIAIAKSCAMIVAADFIP GNGIPVDSVVIDRKINPLQIKQD GGKALKLLVLWRSDEDAQQRL DMVKEFNELCHSHGLVSIIEPV VRPPRRGDKFDREQAIIIDAAKE LGDSGADLYKVEMPYKGGPQ QELLCASQRLNDHINMPWVILS SGVDEKLFPRAVRVAMTAGAS GFLAGRAVWASVVGLPDNELM LRDVCAPKSGEPIL
29520	59888	A	29702	294	479	KIHFGFFCHCAESGSLDGRHFA PGV*RSEQHSGSGAVSGTGY WCSRDYRSREIDGLYRNW
29521	59889	A	29703	1446	2103	IHTDHRPGEIAATTLANRAALS GAALRRRRRQNTIAVGVRLA GTAHACNIIISIRGYGSDA/Q/ QRLDMVKEFNELCHSHGLVSII EPVVRPPRRGDKFDREQAIIIDA AKELGDSGADLYKVEMPYKGGP GPQQLLCASQRLNDHINMPW VILSSGVDEKLFPRAVRVAMTA GASGFLAGRAVWASVVGLPDN ELMLRDVCAPKLQQLGDIVDE MMAKR
29522	59890	A	29704	370	1080	
29523	59891	A	29705	547	928	RLTKVEMPFYKGGPQQLLCA SQLNDHINMPWVILSSGVDEK LFPRAVRVAMTAGASGFLAGR AVWASVVGLPDNELMLRDVC APKLQQLGDIVDEMMAKRFP LLRRWVDLALTRWLITVSKP

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29524	59892	A	29706	1	550	MESGVATRPADFDVYIDKLTE FVYKTNLFMKPFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILJGRPNVIEMRIQKLGLOI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVQTQEQARALIS NPTVIGAIMVQRGEADAMICGT VG DYHEHFSVVKNVFGYRDBGV HTAGAMNALLPSGNTFIADTY VNDEPDAAELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTVPVLMGVAKP VHVLTPIASVRRIVNMVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRYQHGVVTLRFSG CFFAFHRHINAVFRFNIQAVFV ALRPEVIAMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIVQH VLQAEGFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTPLWAWLKLW QRIDEDNMTTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFIANFLPATGDVIRQRYE QFVANSNKMTAVGAGSQGDQF LFALFNCQCFDADELKRIKNEL EPKMGMEMLNLVQLIAYTDWNE TQQQKPDGSWVNNYNDWMFK
29525	59893	A	29707	898	1163	
29526	59894	A	29708	81	454	NRLLAGRISSGTGDHFSGAAGI DSSLRPVW**TLRDQMSGGQS AKQPGRFQWFFYP*RLPETG*V PE*CL**CELIRAN/DHFLVSILPL RSPCVPLHLSTTPLRLAMDLTG LSGFPIPLSQSA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	1	2218	
29529	59897	A	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	C	29713	1	3126	
29532	59900	A	29714	642	825	

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29533	59901	A	29715	107	1315	KCADLPVRGLRHCWRRREDPS GADRSFSAIHSGRAAFWPCR* QGALMSIEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSQSPRSYS VLRSKFDAWLMEQAEAGAQL ITGIRVDNLVQRDGKVVGVGEA DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVAVGVELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNT LSLGLVCGLHHLHDAKKSVPQ MLEDFKQHPAVAPLIAGGKLV EYSAHVVP EAGINMLPELVQIP CIERNAINAVKANNAARMAMR RTSAPRVSLDKVIETMYETGKD MNDKYRETSRGG LAIKV
29534	59902	A	29716	3	264	
29535	59903	B	29717	85	737	
29536	59904	A	29718	171	820	LGVCAMTNSQCG/CDEYRSKN GYEGARKALTGLSPDEIVNQVK DAGLKGRGGAGFSTGLKWSLM PKDESMNIRYLLCNADEMEPGT YKDRLLMEQLPHLLVEGMLISA FALKAYRGYIFLRGEYIEAAVN LRRAlAEATEAGLGKNIMGTG FDFELFVHTGAGRYICGEETALI NSLEGRRANPRSKPPFPATSGA WGKPTCVNNVETLCNVPAIL
29537	59905	B	29719	1	486	
29538	59906	A	29720	1	605	
29539	59907	A	29721	285	449	TPAARDAQLSGGRGWY*CSAG NGLMQHRSQSGDWRAGRPFTE GW*PTPDWQIEA
29540	59908	A	29722	411	557	

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29541	59909	A	29723	1244	3261	KTINRTSLWYWLHDHWSVTG RCAFTDVTKVVDHHEPQTQTR GLVMTTS*ATT*KLTVSLTTAC VMNWV*MQVIPSPPTAKIRL*LR TSNWLTSITTLTT/NNDVNGDSI DNGTEGSAVRVGLGTQFSFTK NFSAYTDANYLGGGDVDDQDW SANDLTGITAKDAQMLSVVKP LQEFELFVLALESRGTLADILK AAGATTANITQAIQMRGGESV NDQGAEDQRQALKKYITDLTE RAEQGKLDPIGRDEEIRRTIQV LQRRTKNNPVLIGEPGVGKTAI VEGLAQRIINGEVPEGLKGRRV LALDMGALVAGAKYRGFEER LKGVLNDLAKQEGNVILFIDEL HTMVGAGKADGADAGNMLK PALARGEWHCVGATTLDDIAS TVKRCWTSHQHQTKNRTRRT TRNIRFPNQMEQINIALEQKGS GNFSAWVIEACRRRLTTGGPHV MYVLHHADKPNLYHGLPENPE ISETVKFWKGIWKPLAAVGF TFAASIFHYERVIFLTGQVEDH MANLJIVQMLFLEAENPEKDIY LYINSPGGVITAGMSIYDTMQFI KPDVSTICMGQAASMGAFLLT AGAKGKRFLPNSRVMIHQPL GGYQGQATDIEIHAREILKVKG RMNELMALHTGQSLEQIERDTE RDRFLSAPEAVEYGLVDSILTH
29542	59910	A	29724	1487	1821	QYRPESVLEDPRRSDHRRITDS FRETSFIVQSIVCRVLSRAILQS KRL*EPGEFPPDPSSPEQRWPV CYPK*SDR*PEYPHSPGRQES QSRYLPAFRHRYYSQTTAY
29543	59911	A	29725	4063	6544	
29544	59912	A	29726	174	556	
29545	59913	A	29727	1	1926	
29546	59914	A	29728	1	1443	

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29547	59915	A	29729	1	817	MAFNEPLMLEPAYARVFFCAL AGQLGITRLTDTVSGITLDAGQI AEPLALFGEDDDMDPRPSRYQ VANGIAVLPSVGTLVSKTRALQ PYSGMTGYNGIARLQQAISDP GVDGILLMDTPGGMVSGAFD CADIIARMRDIKPIWALANDMN CSAGQLIASSASRRLVTTART GSIGVMMMAHSNYGAALKTNGV EVTLIYSGDRKV\DGPNPEKLP KQVRADFQTRIDATR\SAYTGM SVQDV/LDTEAAVFSQGQSWDN GLAE*LVHTDWL
29548	59916	A	29730	68	98	
29549	59917	A	29731	215	871	
29550	59918	A	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP EQRDAGRFCSLAKETVTPQW *GVLTSIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLGYSLVCSRVLAC FWPGSDFWPSRRKTSHTVEA FPV/VVIFVSWRNPQVAPTSAH QNRPSRNPVSRPPNTQVRARR HYALADGY
29553	59921	A	29735	403	588	
29554	59922	A	29736	1	743	
29555	59923	A	29737	5	97	
29556	59924	A	29738	756	935	
29557	59925	A	29739	1	1056	
29558	59926	A	29740	1193	1405	
29559	59927	A	29741	1	2718	
29560	59928	A	29742	3	357	

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29561	59929	A	29743	3	1307	KYGFVHYTLHTLGGTARALVA TDYRPLTKLSLDNGFQTVVDHLQ ISQCPYIPPNFPTDTSPTGGLL QPPEGHAYDAYWRCVRAVRG QRVSALHGPPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YSGSVRSWVQPGGFARYKYDQ TGNASTVKCDYYRMAAFGHH AYRMQALTCSMTACPTTRQE TSSAWGSVSSMGDSRPPQEILG QPLLGRRIKYNCTGIGPWDGKG DESGASRPKQQAAGWLWACP RIFLVIPHSSHPAARTNGSVGG SNRNRFVIITGPGQLAPKGLW QWPIGQDPVTEIATLIGTHDLIM FDCIGVSAPTQPLEKLLSIVRY PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVFTSAF APVAVTAPRQSRQFPRLSPL DAHQRMGDVSIQAVKEARTC

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29562	59930	A	29744	1	2352	MLPDSSVRLNKYISEGICSRRE ADRYIEQGNVFLNGKRATIGDQ VKPGDVVKVNGQLIEPREAEDL VLIALNKPVGIVSTTEDGERDNI VDFVNHSKRVPFGRLDKDSQG LIFLTNHGDLVNKILRAGNDHE KEYLVTVDKPIITEFIRGMSAG VPILGTVTCKCKVKKEAPFVFR ITLVQGLNRQIRRMCEHFGYEV KKLERTRIMNVSLSGIPLGEWR DLTDDLEIDLFLKIENSSEVKP KRRPNRKQRASNVQSLRWKKR RKKAVARRPTQSSDDAIRGQQP DGVDCRDCRAGERQRQQTDSA MMELMVVHPHFVLSLGGLLL AAEMLGGNGVLLWSGVAAVIT GLVVWLVLPGWEWQGVMAFI LTLAAWLVWKLWLSRRVREQ KHSDSHLNQRGQQLIGRRFVLE SPLVNGRGHMRVGDSSWPVSA SEDLGAGIRQCQLVAHGLQLL NVSFDLRLHFLQGRLEFGCALR LLTDSQSLRSRPRGWRGLYG YSPPCGDIVRYHHHDLVSATLH VHINHDDCLEIAVLKQDGMGDV QHFADDVIAQRGFFAFSYEDT VIKIEKDFMTSGKPAARQGDM TQYGGSIQVGSAGVRIGAPTGV ACSVCPGGVTSRGPVNPLLGA KVLPGETDIALPGPLPFILSRYS SYRTKTPAPVGSGLGPGWKMPA DIRLQRLDNTLILSDNGGRSLYF
29563	59931	A	29745	1	3075	
29564	59932	A	29746	755	1321	
29565	59933	A	29747	397	576	
29566	59934	A	29748	1014	1266	
29567	59935	A	29749	416	724	TPGLTKTPCWEKVTFLSLQWS AYRQANTSLGRHSASSLLPLAC RY*R*WRWQKLAALVTASARQ SVKSLAYCWQRFTWRWGRFS LRRVQLPFPLKWGLRR
29568	59936	A	29750	230	1829	
29569	59937	A	29751	1	474	
29570	59938	A	29752	137	586	KTKTNIKL*AAPITRMVMVRHA VHSGSVKK*SDITMSFATISVIG LGYIGLPTAAAFASRQKQVIGV DINQHAVDTINRGEIHIVEPDLA SVVKTAVEGGFLRASTTPVEAD AWLIAVPTPFKGDHEPDMTYV ESAARSIAPVLKKGAL
29571	59939	A	29753	2	557	

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29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPPVYT**PTA QGLSARQGCTKGHQVRRYGRF HD
29573	59941	A	29755	66	372	
29574	59942	A	29756	1	992	
29575	59943	A	29757	1	393	
29576	59944	A	29758	1	3753	
29577	59945	A	29759	1	1098	
29578	59946	A	29760	320	703	
29579	59947	A	29761	2	673	AAFLRECKDPQTMVPAKINSVI WRIGLFYVGSVVLLVMLLPWS AYQAGQSPFVTFFSKLGVPYIG SIMNIVVLTAAALSSSLNGLYCT GRILRSMAMGGSAPSFMAKMS RQHVPYAGILATLVVYVGVF LNYLVPSRVFEIVLNFASLGIIAS WAFIIVCQMLRKAKEGKAAD AHFTPYHATPLRNVMHLIYVLN GVSFRFSVIDTNQIAQRNRFAL LCGA
29580	59948	B	29762	51	623	
29581	59949	A	29763	1184	2406	
29582	59950	A	29764	103	473	
29583	59951	A	29765	444	699	CWPGKMSWGGFPLFLGIGVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVYSGIQ LLPGLVLGGCMCRGIYA
29584	59952	A	29766	3073	3621	GVDNWRHPIHISARLQR*AGSFFS FLGETGSLSCGLSLFSKSCCEAK NCSGSRGSSP/G*IPGVQEWNI FSRF/HGVGLASLRKQAPGDQ SPITGLLGE*AHGEIPVGNRSG KTRA/RGGPRGLEVSWSGLTH SRG*ASLTSSHNSCHIRRHGPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29585	59953	A	29767	362	1850	
29586	59954	A	29768	1	1401	
29587	59955	A	29770	1366	1515	YDQAEILDQIHGSSSN/EQDPR/ RLPKGLTPQTLR/TLCQWIDAH QDYEFSTDG
29588	59956	A	29771	1	1827	
29589	59957	A	29772	419	1295	
29590	59958	A	29773	167	451	
29591	59959	A	29774	94	304	SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
29592	59960	A	29775	345	652	
29593	59961	A	29776	596	2297	
29594	59962	A	29777	184	283	

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29595	59963	B	29778	16	1058	
29596	59964	A	29779	715	1234	FTWIGFYANRHFCHPVTNDP HFMKWRAAAHGGENIAFKLAN LPFFGDIRESHYQVVINRADRG FNPDDFTGARQQKFVLIAGGF P*QLL*TNAVIGREFRNVQECIG LHTAGFANAVTKHF/W*M/PRL HCTIWRSGSRITIGRSRWSTAI NCRVCSFCAISTLASRTSAR
29597	59965	A	29780	938	1250	PGRVSGKADGSV/LAGNGLLP FFCPLRLRGKYQPEV/IASTIRRR YQLLFLAVASHQATAAGCGVN ALSDLRLCSVCRPDKTHSVASG NGCRMRLPSSPFSVL
29598	59966	A	29781	1	1389	
29599	59967	A	29782	3059	3537	SEGKTANLFNKAITCSGAGECT RPWASDIKAQCAGGISRFATGN GFKRLCDTLRYLQAIENGLKN WRLIHIATVRRCPPT/LSPATID AINVIGQWLAQDDFSGEVPYQ ADCVLAGNAVMPITDAACKIA RDQQLAEGDFGLRCEIRDWCA NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVLVHHFH AITHIRQQSQITRYIKLLRHRH TQRRFTACRLRVDAPFPNGHQC CALHCLRKIDRIQHNFNARNFIR IEKYRRRNTHTRASAA/DPSSGR H*FQFAVVVKHGRNFAAPVQVL RPSPALPLFAGQTTPPRRVPLPA GYQRHMLLQYDQATVN
29601	59969	A	29784	269	753	YRTPTLQLDQGRADARRGVW/ HVPFSHESV/WENIVMTRQAQG ANFT*TLFCFGIGFAVIA*NCAI DPDISIRFFSKEETAT/GDRPDQI AAHLWRFPTPGGRFVHHRGAY AAIIFRP*YLNGRSMAEQSMILV TGELLVELNLEPSQVQNEFAEK YYGPASQVV
29602	59970	A	29785	762	1182	
29603	59971	A	29786	3703	5889	
29604	59972	A	29787	925	1130	
29605	59973	A	29788	658	1212	
29606	59974	A	29789	904	1473	
29607	59975	A	29790	1205	2222	
29608	59976	A	29791	1	194	
29609	59977	B	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	

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29613	59981	A	29796	1	738	MQPWALPTV GELWVCGRPGA ALRAGTEPSSRALGVSETALPA EIKLRVIRVGHSSPLAQLASFQK PVLVFLRLNSRRFLFLSLARSED GILFAKSKHSSPLSLTPLRCIVL MRMYEQLMSGDLQCRVMMP RNNPGYWNQ**SEIFKGSQAQ TMATLTCSEFKKPPKIPYKAIAL ATVFLIGAFLLIIRLPSCCQGYI KQRRGGRPGPQLLIIGHSWCSY PGFYPPAHRFTMHFKGLPVVN PNE
29614	59982	A	29797	1	186	DCRLRAGDPRRSHCAVSPGTGGS RALSGYRY*SVDPQRNDGVDQ *ATLRASAHLQTAVVEFSA
29615	59983	A	29798	724	1015	RSHPQCGYLQNHTSSASFSA RKG*NRHYAFARNDRLVAPCS HHHQ*PAPAPVHLH*PVDLST AIDAPAVNGDGKARPSKRRYQ RLSVPEVVQY
29616	59984	B	29799	1	4182	
29617	59985	B	29800	1	1191	
29618	59986	A	29801	167	504	
29619	59987	A	29802	1541	1852	FALFANRVSLAANVSGRGSPC WWRRIAVVCCSTNR/RSALDIA HQVDVLSLVHRLSQERGLTVIA VLHDINMAARYCDYLAAPCAA VK*LLRERLRKLCAAKPSK
29620	59988	A	29803	407	3584	
29621	59989	A	29804	3	150	
29622	59990	A	29805	1	921	
29623	59991	A	29806	300	560	IRDKNRVFLRESWRRLFTTAND QPHRPARRIISIAGIKWRYSDFLI NYCAGRAVF*RETGSVVERWH HHAGWKTPFRKRAGRTAGH
29624	59992	A	29807	100	315	PIKITSALASARYVRATLSCSR NSTLRWKK*RKMLTKPSTTN GSRSNS**MNFFL*QAPPG*PSA LPFVH
29625	59993	A	29808	3	116	
29626	59994	A	29809	1	1469	
29627	59995	A	29810	1	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYQRA CSGR*VPNLRLPEVQSTDRLLS QRRRVSPDRQWWLACH
29629	59997	A	29812	438	1942	
29630	59998	A	29813	1	1464	
29631	59999	A	29814	3	602	

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29632	60000	A	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA SVVSRDGFVIAGGGGMVVVEE LEHALARGAHYAEIVGYGATS DGADMVAPSGEGAVRCMKMA MHGVDTPIDYLSHGTSTPVG VKELAAIREVFGDKSPAISATK AMTGHSGLGAAGVQEAITYSLM LEHGFIAPSNIEELDEQAAGLNI VTETTDRELTVMSSNFGFGG TNATLVMRKLMIISASTSILR
29633	60001	A	29816	1	2472	
29634	60002	A	29817	1	469	LFNREVCCLGQGQS*QMAL*LL GIESYIT*L*SGGDN*ASIGVIPDP AAIAR*RPWRSACG**PKCPLA DVFAGHSGRKRPPSMAFTATLI SPGTGRRAINSULAQFKAGESNI WLSALPTPLPTTIRITNGALPSTF SGSSTFARISPISSFSRP
29635	60003	A	29818	884	1084	
29636	60004	A	29819	1	1040	
29637	60005	A	29820	2711	3854	
29638	60006	A	29821	1	957	MKIGTQNQAFFPENILEKFRYIK EMGDFGFEIDGKLLVNNIEEVK AAIKETGLPVTIACGGYDGWIG DFIEERRNLGLKQIERILEALAE VGGKIVVPAAWGMFTFRLPP MTSPRSLDGRKMVSDSLRLVL EQVAARTGTVVYLEPLNRYQD HMINTLADARRYIVENDLKHV QIIGDFYHMIJEDNLAQALHD NRDLLGHVHIADNHRYPQGS TLDFHALFEQLRADNYQQYVV YEGRIRAEADPAQAYRDSLAWL RAGQVADKVHASYYCTRDLE LVAVCD SRLSQAQALAEKYG ASVWDDPQAMLLAVKPF*FVGL VIGAGQVADKVHASYYCTRD LELVAVCD SRLSQAQALAEK YGNASVWDDPQAMLLAVKPDV
29639	60007	B	29822	96	821	
29640	60008	A	29823	3	775	
29641	60009	A	29824	961	2073	
29642	60010	A	29825	1	849	
29643	60011	A	29826	319	541	
29644	60012	A	29827	1142	1756	
29645	60013	A	29828	44	283	
29646	60014	B	29829	1	1812	
29647	60015	A	29830	685	1146	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29648	60016	A	29831	202	918	AVDVTGLADHRDRTEHGGAFAA IVHRIVKHFITAWAICQQRNHA ALVVIRRLLEANHRRHRTGRG/S VDRVSAARSLSSGTMPPGNGVW RIGVFTQLSVA/WHQ*VDLLIVF QFVRDTTIDDDHVGIFALAAAND RAAFDNILDPTGSVDVLLPLPG RHNIANALAAAALSMVSGATL DAIKAGLANLKA VPGRLFPIQL AENQLLDDSLVNAAQQNLS VHILNQQTGKPAADVTVTLQE
29649	60017	A	29832	1184	2409	TLKACCLVRSMCRVAVP*RC/GR QLVSSDNISNDPMNVIDWINMY ALAVSEENAAGGRVV TAPTNG ACGIIPAVLAYYDKFRPVRNER SIARYFLAAGAIGALYKMNASI SGAEVGCQGEIGVACSMAAAAG LTELGGSPAQNMEGKIDRPEE YADIATKCVTNFREKNRDRCL VILSRNDEALNSQRTSEELHHY YEIVWDEEQTHKFNISPHLQRI KAFKTLGGPHGNITVDMVISAQ ELLQEDMATFDGHIVEALMKM PEVNAMYPELKLHAIGWVKHK CIPGAKWPEIQAE MRIWKKRRE GERKETGKYTSVVDLARARAN QQYTENSTGKISPVIAAIHREYK QTWKTLLDDELAGRCFADRQN LMVCLRSMNPVFTGSCARMRC CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA MIPNFWAFLGVTTWIFMAAG GAESVA/CTLTTSKAVRNR/SFK* SSSPGILSGYVSRSSGSPISLISP ASLCAGHMRFFCSSSKPTCSNP RTFAAALSSAWSSPSPNEGFSSN PAFLGTSLLMMFHLELRRCIPIV TTDLLPLTSGDVGLVLLCVGLD GSLWSDCRMTESVSTNTTPPIIT SRNS
29652	60020	B	29835	46	893	

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29653	60021	A	29836	3	2037	CTSSDPDPSGLPPGFAKLTSLHVT LVEVGVSPEPDEGWLYLAVID LWSRAVIGWSMSPRMTAQLAC DALQMALWRRKKPRNVIVHTD RGGQFGDRWKGWLTSTRIFRWI SFQPALAPTRKAALCYLAREVN PDMADYIKKLLPGIHVREESR RYYPSGEVTAHLIGFTNVDSQG IEGVEKSFDKWLTGQPERJVR KDRYGRVIEDISSTDSQAHLN ALSIDERLQALVYRELNNAVAF NKAESGSAVLVDVNTGEVLAM ANSPSYNPNLSTGTPKEAMRN RTITDVFEPGSTVKPMVMTAL QRGVVRENSVLNTIPYRINGHEI KDVARITTEEDFNHASAARFVC AAAERCKTTINLVPENEVLNV LEGEDAETNALRAKRRCPKCG TAMDSYLIDPKRKLHVCNNP TCDGYEIEEGEFRIKGYDGPVE CEKCGSEMHLKMGFRFGKYMA CTNEECKNTRKILRNGEVAPPK EDPVLPPELPECKSDAYFVLRD GAAVAARFNDDRHRRLGLAVLY ADQADLYGVADSVSAGDSL LYKHERRLVPLLVSSLLFLY RHGIRLPCGSPGGIWAPWQIRR GRQAVNCLAPM/HHPGKNRAW KTYCSQ*AIVPQLPVCIGI*PRSD SYHDYQRDPRCQPLRALWRRS DSPIGGYSSAIGI*TERHCRSGNP
29654	60022	A	29837	993	1832	
29655	60023	A	29838	124	276	QEGRCQVTITRKMPLSSDLGSL HGLAGNHISPPICARTPHVATVL RQLELEDKHWNGSG*FARLG WKPSPHLCQNPPCGHCPQTAP GA
29656	60024	C	29839	64	267	
29657	60025	A	29840	3	86	
29658	60026	A	29841	1	1481	
29659	60027	A	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK*VGGSSRVNVPPQVFI SLVSQMFSENDLPLVRKRKTEP
29661	60029	A	29844	115	903	
29662	60030	A	29845	1194	2311	
29663	60031	A	29846	368	502	
29664	60032	A	29847	1156	1359	SEPVPYLCYLRQLAVQANPRR MRCIARHFNINGNRHLTTTINFI *SMVSLIANRLIIDLIHTVDFY
29665	60033	A	29848	1	228	

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29666	60034	A	29849	102	296	YRNSHNLLQGWFQIHRGDLLEYH SSPHSR*KHRNRHNARARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	A	29850	1	4185	
29668	60036	A	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVVIDQCVFLIRV TNPAGSFFELRH
29670	60038	A	29853	2	834	
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNNLVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	A	29855	1591	3150	
29673	60041	A	29856	2	222	
29674	60042	A	29857	16	359	TTHKTRWQAPVPLRGSPVVAL RIPSDQSEAV/HLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLFFNRHYICFTRI RRFRWHRSSLFHGMNVKYRRS KINN
29675	60043	A	29858	207	470	ATIL*GDFYP/GSRNWLGVSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTSGHVLGSCCV NGKTLRKSDSRWQQLLRSLIR R
29676	60044	A	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCMAIRSPIRMASSR SWEIKTMVR
29678	60046	A	29861	593	1881	
29679	60047	A	29862	3	198	
29680	60048	A	29863	1	1590	
29681	60049	C	29864	1	5421	
29682	60050	A	29865	63	185	LCQSHAPRKFPARPFRRFR*RQD CQTSVFLLRPVANRAPA
29683	60051	A	29866	1	715	
29684	60052	A	29867	1	1212	
29685	60053	A	29868	886	1185	
29686	60054	A	29869	190	433	AFAKLFIMAAALTSQVAHLSSS GTPFRPFCLPSC*LSSSRAAIST CSLYAAWFPLTLIRCGIRKSPII CGISRCRCWRQ
29687	60055	A	29870	1	439	
29688	60056	A	29871	14	106	
29689	60057	A	29872	2518	3024	
29690	60058	A	29873	448	537	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29691	60059	A	29874	463	889	FFGLVTSSPSADSPAMLDTRNV SHTGLGPIIPLTFEAGIHTRPTPN SPPRSCLAPAIKA*FFSPAARITT CCASLYRSPLKTLRSVRFWRSS ASVLMRRSSSAAPMPEATI.RVL SGLRGSRSDDKAFTPHPTI*CLEA FPGSRAVFASAP*CLTLRANQR KGCW
29692	60060	A	29875	524	1006	SLLAWSGINIFASSRIAIASPLA ASVPLSMDNISLCTPSGVPEKV TSTVLTSVPQSCKLMMKDFSGP *FP*EKRVSETSPNCTLICLLSCA STHVI.RRNDPLMLTVPWSWANS SQPHVNPKNRIQIIPFNITPSLV NQIKIETRRRAFTPLPLCGLITK
29693	60061	A	29876	2005	2517	
29694	60062	A	29877	1	470	MQRDGDIALIYRSKIGPRTSIT FTARRANPVQRIARILLRDHLI CRMSCTAARHANTFDLIQGGG ADNFAAIYGGANDRITRADA/V SRGCWKLAPVRDIKRQTVAAF YHQDIQPGSCHDQNAL*STGFW REQSGGQ*P*AG*TSNRTRCCIT GR
29695	60063	A	29878	734	1306	
29696	60064	A	29879	743	901	
29697	60065	A	29880	771	1013	RLGTVGTDLSWCYQYQLCYQ* ALPFSTLPAGLAGNGCQRRRCA GTHSLWHADLSVWPDADSLF QRDGRAGGGATRLLR
29698	60066	A	29881	1094	1345	
29699	60067	A	29882	2	751	
29700	60068	A	29883	239	483	PTPQHLYHALTGSTIMSQRGV DIPCHWHDITCGHAHSLPHRRG RKA*SMGNN*YSCTWCYCEGG TEKAIWPGDGCPLSV
29701	60069	B	29884	228	803	
29702	60070	A	29885	488	636	
29703	60071	A	29886	1	2117	
29704	60072	A	29887	665	795	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
29705	60073	A	29888	1743	2013	LQCTQYAVGENPAVNFAGRPK GSPCFPGGGGLN*AAADIPVAS DNPAHYADAIRYNARTPLQAG VYFVRDGPGLASVRNKERYF ANNYIYDMGRNKDGRQSTWY MGLGTDIDTGLPMSLSMNYYA KYQWQNYGAANENEWDGYRF KIKYFVPITDLWGGQLSYIGFTN FDWGSDLGDDSGNAINGIKTRT NNSIASSHILALNYDWHYSVV ARYWHGGQWNDDAELNFGN GNFNVIRSTARGWLPGTICRPDK MRQHRIRHCAPIAGCGTGCRPD KTRQASHQAQMSNAYDYSEIQ PPSEGEILLDAQPLESWSSKAFA RKVAYLPQQLPPAEGMTVREL VAIGRYPWHGALALLGAADRE KVEEAISLVGLKPLAHLRLVDSL SGGEPGVDRLVAQDSRCLLL DEPTSALDIAHQVDVLSLVHRL SQERGLTVIAVLHDINMAARYC DYLVALRGEMIAQGTPEAIM RGETLEMIYGIPMGILPHPGA APMNTAHHAAIDPNRIVALEW LPVELLLALGIVPYGVADTINY RLWVSEPLPDSDVIDVGLRTEP NLELLTEMKPSFMVWSAGYGP SPEMLARIAPGRGFNFVRNTP LARTLQLJLREGPRGHPALVQV VDLLIEPPQLPLLVPVQTRIPRI QPQSHPAHGVNEAVRNPTVWV APFIDEIHSIHKYSI
29706	60074	A	29889	1	1584	
29707	60075	A	29890	1	1188	
29708	60076	A	29891	728	970	
29709	60077	A	29892	2447	2665	
29710	60078	A	29893	255	1360	

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29711	60079	A	29894	1	1890	MYSRFDIVVAEPICTLTTFGKET VVSDSQTRTTTTDDPLQVLQV LDRADIRPTTHNEDLPFGGALG LFGYDLGRRFESLPDIAEQDIVL PDMAVGIIYDVALIVDHQRHTV SLLSHNDVNARRAWLESQQFSP QEDFTLTSDWQSNMTREQYGE KFRQVQEYLSHSGDCYQVNLAQ RFHATYSGDECQAFLLQNLHGN RAPPSAFLRLQGAAILKLSPERFI LCDNSEIQRPIKGLPRLPDPQ EDSKQAVKLANSKADRAENLM IVDLMRNDIGRVAVAGSVKVP ELFVVEPPFAVHLLTITATQLPE QLHASDLLRAAFPGSGITGAPK VRAMEIHDELEPQRRNAWCG/SI GYLSFCGNMDSITIRTLTAING QIFCSAGGGIVADSQEEAEYQE TFDKVNRILKQLENYRRALRDL KEEVAILRSPFELSFAFCSPSIASM ATRYPNGRHIPDDLRLPKERGIII VFTGNGKGKTTAAFGTATRAV GHGKKVGVVQFIKGTWPNGER NLLPHGVFEQVMATGFTWDT QNRESDTAACREVVQWAKRM LADSSLDMLVLLDELTVMVAYD YLPLEEVQALNERPHQQTVIIT GRGCHRDILEADTVSELRPVK HAFDAGVKAQIGIDY
29712	60080	A	29895	159	475	VKVNLPWAMLLHSGYADHPYS RFDIVVAEPICTLTDT/GRCSHIS LYAAGIINSDSKGAVIMPPIIGA AIRLITSEPAVPVPHRIGSRPAIITA TVIAFGRTRRTAP
29713	60081	B	29896	158	810	
29714	60082	A	29897	1	2070	
29715	60083	A	29898	1081	1218	
29716	60084	A	29899	289	1014	
29717	60085	A	29900	145	297	
29718	60086	A	29901	452	568	
29719	60087	A	29902	21	185	VHDQPSQEIQQRTEAPGRSS RRVAQCHPQPGES*SRAQIPPAS TPKPGGGDL
29720	60088	A	29903	1	711	
29721	60089	A	29904	2	825	
29722	60090	A	29905	812	961	
29723	60091	C	29906	1	1587	

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29724	60092	A	29907	3	403	LVFDDGDVQMGFWCGCPFCLL VFLLTVRSLSCRSVGVCRSTR DLVCLGISSGGCRTVNIAEQQM LLPDCSSGIFVSEGYLAV*GVSL PLLGGASQLGLGSMAlFMIILP IHEHGMFFNLVSVSSILLSSCL
29725	60093	B	29908	168	863	
29726	60094	A	29909	340	612	
29727	60095	A	29910	1	834	
29728	60096	A	29911	92	548	
29729	60097	A	29912	1251	1682	VPVALAAARRSELSRTAAADT G*SAAAEVLNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGGQSSWAPFEWEGAPR GEEWTLVSVGALK
29730	60098	A	29913	1	1278	
29731	60099	B	29914	1	2007	
29732	60100	A	29915	406	615	
29733	60101	A	29916	52	391	SNRLKLMHSSRSSCMFFSSIR SFKDFSLVFDGDVQMGFWCG CPFCLLSFPF*QSGPSAARSVGV CWRSTPDPVCLGVSSRGCTV NIAEQMMLPDRSSGSFVSEGY PAV
29734	60102	A	29917	759	1190	VPVALAAARRSELSRTAAADT G*SAAAEVLNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGRRSALGQLEWQSGQ SPAGAAIAAFDNR
29735	60103	A	29918	84	3661	

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29736	60104	A	29919	1	1230	MDAGWSDVGSWSSLWEISAHT AEGNVCHGDVINHKTENSYYV AESGLVTTVGKDLVVVQTKD AVLIADRNAVQDVKKVVEQIK ADGRHEHRVHREVPWGY DSIDAGDRYQVKRITVKPGEGL SVQMHHHRAEHVVVAGTAK VTIDGDIKLLGENESIYPLGAT HCLNPGKIPLDLIEVRSGSYLE EDDVVRFADRYGRGNDMKKL TCFKAYDIRGKLGEELNEDIAW RIGRAYGEFLPKPTIVLGGDVR LTSETLKLALAKGLQDAGVDV LDIGMSGTEIYFATFHLGVDG GIEVTASHNPMDYNGMKLVRE GARFISGDTGLRDVQRLAEAND FPPVDETKRGRYQQINLRDAYV DHLFGYINVKNLTPLKLVNSG NGAAGPV/VDAIEARFKALGAP
29737	60105	A	29920	1	1398	
29738	60106	A	29921	426	1861	
29739	60107	A	29922	863	1388	EPERTSIKSGIFPGFSRQCVAPS GI*MDVVFVKQFDITINGDFCRS RDNHPVFRAVMVHLYRQALAR FHGDFAHLVAVARVDRVIFAPR TIHFAMHPMLMATIGFDLLDHF FHILYRVTVGNQHRIFGLHHYQ IFHPDGGDQARFSIHIAVFSFVIN HIAVANVALGGVADLP
29740	60108	A	29923	1	2055	
29741	60109	A	29924	1	2047	
29742	60110	A	29925	1	1294	
29743	60111	A	29926	1	1020	
29744	60112	A	29927	1	1422	
29745	60113	A	29928	1	1698	
29746	60114	A	29929	210	340	YGDVEHESWLSVVRHAHPRIP FA*PTLISLQKRLGKWSGVTGA
29747	60115	A	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK GYGHHYRNL/PVNGPPLSL P*YCKAKFKPSTSQVP
29748	60116	A	29931	63	281	
29749	60117	A	29932	345	467	LPTRCTYTNLTRRSPPAWYY* *YWHRDICRSTPARRQTE
29750	60118	A	29933	29	281	MFGKELGRRDVSQLGAAEITYI LKD*TES*EILCGGRFLPLRG RTLQGGEWPSLYFHSDCSSHAE QCLLYGFADWAPLAFFR
29751	60119	A	29934	520	714	

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29752	60120	A	29935	222	527	LPSKLSAGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAELGHLI SFLHALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGSLSPDIEG DLIQGQRHRDHIGP
29753	60121	A	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRRVLLIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSYLDALNGGD AESAGLTPPELWPRHHGHGPA GVKLVEQLCQRLRPVNEIRDLA RLVAEFHDLIHTFPMNLNPKTIV KLFDSDAWRKPQORVEQLALTS EADVVRGRTGFESADYPQGRWL REAVEVAQSVPTKAVVEAGFK GVEIREELTRRIAASVSWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVFSLREQIRSHEIRRSAVS NHQHFRACGHIDRRTVQTLA HLTFRFGDKGVTRPDEFVHFV HRFRTKGDPLLTFWPSAPVTAT ILRIPLANGFFRHDHKSSCMTR VPQVPEDPVKSHAPQQFWIHH GKWFAYWDVAIGIPGPFAGRS\ CVILLGDAVREVTRVSNVPAK RYIGGSPRRGFINSNCMPGIISPG
29756	60124	A	29939	1	114	
29757	60125	B	29940	1	4191	
29758	60126	A	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSLSLRAFW ASAPVTATNPPDTLGNQFFRHD HKSSCMTRVPQVRSPTELNRSQ GASRPRGVIIQLGHRDPNGDDS HVRIGLIKHP
29761	60129	A	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	A	29946	1	936	
29764	60132	A	29947	1	966	
29765	60133	A	29948	1	675	
29766	60134	A	29949	1	792	
29767	60135	A	29950	2	929	
29768	60136	A	29951	1	969	
29769	60137	A	29952	1	420	
29770	60138	A	29953	1	549	
29771	60139	A	29954	1	450	
29772	60140	A	29955	1	606	

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29773	60141	A	29956	1	726	MARGNATLPVCGRDVVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLLTGQQTP AFGRRVSGVIECDNLKTCHTSH GSVMAETA VINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRL
29774	60142	A	29957	1	771	
29775	60143	A	29958	1	1491	
29776	60144	A	29959	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDQMAALSRLG NDYRPTSA YERGQRYASRLQN EFAGNISALADAECNLTCHT SHGVSMAETA VINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIERYQLPQS YQRMDFRRRFLQGFCFRFNH HQTGFSPAGANQRGLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVYIAIK PTCWPLDIIIPSCALHRIETEL MGKFDEGKLPTDPHMLRLAIE TVAHDYDVIVIDSPNGLIGITIN VVCAADVLIPTPAELFDYTS LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSVMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGGNSVLRK
29777	60145	A	29960	1	1731	
29778	60146	B	29961	1	3345	
29779	60147	A	29962	1	1959	

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29780	60148	A	29963	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPV NVKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKRKNSPRIV QSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPPLYESLCQYS
29781	60149	A	29964	1	1557	
29782	60150	A	29965	1	2259	
29783	60151	A	29966	1	1959	
29784	60152	A	29967	1	2277	
29785	60153	A	29968	1	2418	
29786	60154	A	29969	1	2028	
29787	60155	A	29970	1	1650	
29788	60156	A	29971	1	1170	
29789	60157	A	29972	1	1446	
29790	60158	A	29973	1	1191	
29791	60159	A	29974	22	1893	

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29792	60160	A	29975	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KIRRKNGPVSATFTSDGKIRLFY TDYSGKH YGKQSLTTAQCDNL KTCHTSHGVSMAETAVINHKK RKNSPRIVQSNDLTEAAYSLR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVYFRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPMYAMRLYES LCQYRKPDGSGIVSL/KIDW/IIIE/ RYQLPKVPSPPEAR/KITRRWRI/V KQRI*LGFLRLSEMPRKQGDY RTRIWKFEGLSNV/LVIQLNKLII ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGVSMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVV YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPMYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRQSNDF*RR GI
29794	60162	B	29977	1	1317	
29795	60163	B	29978	78	215	
29796	60164	C	29979	225	422	
29797	60165	A	29980	1	368	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVYFRPEEDAGD/EKGY ESFPWFIKRIYSR
29798	60166	A	29981	1	409	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVYFRPEKDAGDEKGY ESFPWFIKHSTNITSLWFFSS CTH
29799	60167	A	29982	1	814	

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29800	60168	A	29983	3	678	GSVMAETAVINHHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR YSFPPDYFHGLALNVCGFSRYT VQDVGGSIILGSGGQWLSSHSS SRQCP
29801	60169	A	29984	2	660	
29802	60170	A	29985	179	283	MGQGRNPQTRRTYGCQFRMV K*HGIEMKCEELIL
29803	60171	A	29986	1	643	
29804	60172	A	29987	2	1073	
29805	60173	A	29988	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAADGTVAEYNGYNV VFALAGSPEDADDTSIYMFYQK CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRKIPDGSIVSLK/ID WIIKRSQLPQSAFYQPFMGLRR ESFYFRWERRTLGPLKSFSVVKR GTEAGKFRLAALLVRL
29806	60174	A	29989	1	1692	
29807	60175	A	29990	1	1788	
29808	60176	A	29991	1	960	
29809	60177	A	29992	1	1385	

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29810	60178	A	29993	1	936	MWLVTTLESTDTEHFYHHSK CYWPRALGECILSIEAACQAA GGEAGNGGS AVTKATLGSRRQ AQHWKALARTIRQEKEIKGIQI GKQEVKLLPFADDMIIYLENST DSSKKLSELC DNLTCTCHTSHGS VMAETA VINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPFORALYS CTICNP*ILIPFSVIGLQNRFTQF RLSETKEITNPYALRLYQSLC
29811	60179	A	29994	1	1641	
29812	60180	A	29995	1	1551	
29813	60181	B	29996	90	1515	
29814	60182	A	29997	452	1523	
29815	60183	B	29998	9	2021	
29816	60184	A	29999	1	960	
29817	60185	A	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA SSNCAPRGISPOELTVDLQTKC DNLTCTCHTSHGSVMAETA VIN HKKRKNSPRIVQSNLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQAL KSFAGKEVVFY RPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLNSLFY GVQNRFTQRLNFVQKSRLVD LALKGLRVLLVEGNDPQGTAS MYHGWWPDLHIHAEDTLLPFY LGEKDDVTYAIKPTCWPGLDIIP SCLALHRIETELMGKFDE

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29819	60187	A	30002	1	1756	MPASGNENDLNMPSGTIEIFVR CYVEVERIMDFADFGTTIKQDF RLLGQTSVDRLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRI.ES GHQAPCMKSNNALIVILGTVT DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWYPLCDN LKTCHTSHGVSMAETA VINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQ NFTQRLSETKEITNPYAM/RIPL H*LFR*TLRQTKPDNSAGKCVK I**HTQNQRSGRSQND*RRPVL LASLLGATIDYAIMATTPVLW YPLCDNLKTCHTSHGVSMAET AVINHKRRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYL IPFFIGLQNRFTQRLSETKEITNP YAMQSPYTDYSGKHVGKQSLT TAQVNVSKSDDTL KINGVEDH KTIFDGGDKGTYNQVQFIDEEN
29820	60188	A	30003	1	1653	
29821	60189	A	30004	1	1128	PWISAPVPVDVVEGAMDSVT LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHISDWCCRN GRYPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNREHRTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGVSMAETA VINHKRRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QRLSETKEITDPYAMRLYK/SL CQYRAFNNGGEEKARGKPIL CRYGVGM

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29822	60190	A	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA QRKKKYPPWEKLQGSVRGETP VINHKERK\NSPRIVQSNDFPEA AYSLSRDQKRMLYLFVAQIRKS DGTLQEHGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAKGE VVFYRPEEDAGDEKGYESFPW FIKRAHSPSRGLYSVINPYLIPF FIGLQNRFTQFRLSETKEITNPY AMRLYESLCQYRKPDGSGIVSL KIDWIIERYQLPQSYQRMPDFR RRFLQVCVNEINSRTPMRLSYIE KKKGRQTTHIVFSFRDITSMGFF LESPTQGLASPE
29823	60191	A	30006	233	1538	
29824	60192	A	30007	1	2331	
29825	60193	A	30008	1	1857	MPLRFSSSSRIPYYVNLHKA TGERIDYNFETHSSLEIATD TISDHHPCESAANAETRPSTVL EELARAIQEKEIKIGIQGKEEV KLSLFADDMMIYLENPKDSSRK LLEWIKESNKVSGYKTHVHKS VALLYTNSDQVENQIRTPQFYN SCENKIKYLAITYLTESKDLK RNYKTLLKEITDDTNKWKHIPC SWIVKVAGVESWIHHTQVEVW TPPEETAGSTAHGSDQDQDQPR YTCEPLEDLHLLFQKETSHTIKA STTDPEEKPLPPYKRYCDNLKT CHTSHGVSMAETAVINHKRRK NSPRIVQSNLDEAAAYSLSRDL KRMLYLFVDHIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAKGEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVINPYLIPFFIGLQ\NRF TQFRLSETKIPV\IIEAGLSQSEK QAADGIQGVHAFAFQVCDGCG SSLQHFFLLMLVDFQLPPLLNL RVLIMATLFTIACYVELRGYML HAFQLVSLAMSHLHLAHNQDT HPAISDVLVWCALSHSLFHR SDVRADLSNAYSEEVKFGFLL WGLDCASLHRSDFITSSSETKYH
29826	60194	A	30009	1	944	
29827	60195	A	30010	1912	1915	
29828	60196	A	30011	1503	1961	

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29829	60197	A	30012	1	6552	MAETAVINHHKRNKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQIRLGD GSSRLSMEHGLRSIPAWTLDKFI EDYLLPDTTGFADVKSAVNVV CDFLKERC
29830	60198	A	30013	1	2679	MAETAVINHHKRNKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALK SFAGKEVVVFYRPEEDAGDEKGY YESFPWFIKRAHSPSRGLYSVHI NPYLIPFFIGLQNRFTQFRLSET KEITNPYAMRLYESLCQYRKPD GSGIVSLKIDWIIERYQLPKVPS PEARKITRRWRIVKQRI*LGFL RLSEMPRKQGDYRTRIVKFE GLSNVLVIQLNKLHICVMCLVR DCDVLKTYFHR
29831	60199	A	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI NHKKRNKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSGHINPYLIPFFIG LQNRFTFRFMEQKKSPSNRFT QVRLSETKEITNPYAMRLYESL CQYRKPDGSSIVSLKIDWIIERY QLPQSYQRMPPDFRRRLQVCV NEINSRTPMRLSYIEKKGRQT THIVFSFRDITSMITG

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29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK SESDIHLAEHHKQVLYDGKLAS SIAFTYNAKATDAQLCLESSPK ENASIFVHSPHALMLQILTEQV CTQVVHKPHPEPDSTVKIQNPS EQMAVLYCIVLVGGFEFDLEMN FIQDAESITCMTLEHCDVTC QAEIWSMFTAILRKSVRNLTQS TEVGLIEQCDNLKTCHTSHGVS MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPHYAMRLYESLCQYRKPDGL SIVSLKIDWIIERYQLPQSYQR MPDFRRRFLQDVQNETHGNT
29833	60201	A	30016	1514	6335	
29834	60202	A	30017	2033	4226	
29835	60203	B	30018	1	5670	
29836	60204	A	30019	1968	3130	
29837	60205	A	30020	34	431	
29838	60206	A	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	A	30023	3	1771	
29841	60209	B	30024	1	2299	
29842	60210	A	30025	2	488	
29843	60211	A	30026	1	127	
29844	60212	A	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	1	836	
29847	60215	A	30030	297	936	RTSSSLMRSSSSLLRICSGVSPRS IPRWFTSVSLPSSFIRITTFRYT PGHVAPASRRSCYKYRR*PMRL YTIMQSL/VGSRPSPGLRAFSSD CSPLPRTCSLRRRVLMITTSRS *SLTYGVDPSVRPVLAASEYF SRRYAGFQNPNNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSISCTSTGGNTTL PPSSPPDC
29848	60216	A	30031	1818	1991	SPSHIRRTAPNGLRHRYQR*IQQ* APSDQKRDFLVPHIGADSAMAK HGGSHRAVLPPQGW
29849	60217	A	30032	2	501	
29850	60218	A	30033	1419	1640	IFCASLGLGYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPPQGC DPHMESLI

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29851	60219	A	30034	1	1593	
29852	60220	A	30035	107	195	
29853	60221	A	30036	1480	1605	TILRITTFQCRSNRRRQQR*NRFS STSQRRRCYFLLNGEDVTLTP
29854	60222	A	30037	1	373	MPSYFTSRIAAVHVSALREFQA HHESKHHESFAQRMFRMFYQ ARNLLHAGQENLFSGLTALTAE FTVGEEATRGTGKRGPSPDG RILRTTKTRNPRGYMQGRYLES QRDVEATDKPFEFFMNRFRLL AAPRVEFIAYTGLCEDVIRPQL DEAIAQGYLTCEADYWQITEH GKLFNLNLELFLADGYHMWR MIGAGAHAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPLGIEQ LPALKAFDTVFSMGVLYHRRSP LEHLWQLKDQLVNELVLET LVIDGDENTVLVPGDRYAQMR NVYFIPSAALAKNLWKKCGFV DIRIADVSVTTEEQRRTWEMV TESLADFLDPHDPKTVGEYPA PKRAVSDCAQAVKMTNMISYQ GLVRTLSTSPNNWLVFMQNG QEVVIDSGKSVS*RSVFCGCFIK HGICSMRDKKISFLV*RRLLNS LSAKKLHGAKQRAKGDLPRMG AFCVPPKRVIRVICKEGIWKA SVMSKPKQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCP PSRRQRRRSGPLPEPAPRVS*Q IFPSQYWRYSQSTENQKQRLDP RGQIVNVPARRIIRQKRCKKV AGSA
29856	60224	A	30039	1	1090	
29857	60225	A	30040	1	1384	
29858	60226	A	30041	1	1377	
29859	60227	A	30042	2268	2684	RCRRCKRLLRRFRRLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCCHG*QRC SSDGRKITSVHRGRNADGRELT HQAVALLAYLSDRFARHHRHL RNAHRRGPDRIKERHFPAATKL RHTPAV
29860	60228	A	30043	1130	1310	RLDKQNRGRQGRQNRNGVFHQ QPQR*RTDVIQMPHSHRHA QRDHDQQLGQHAGRNFE
29861	60229	A	30044	395	689	VAAVSSSMSCAPVLMTVVTR CTLLILSQFMRRKAIAK/LSGSL LPASEVKVLKRDGDYSE/VQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPPQGW

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29862	60230	A	30045	1	2142	
29863	60231	A	30046	1	2463	
29864	60232	A	30047	1	1066	
29865	60233	B	30048	790	820	
29866	60234	A	30049	3	126	
29867	60235	A	30050	1853	2257	
29868	60236	A	30051	90	411	
29869	60237	A	30052	1375	3174	
29870	60238	A	30053	5	206	
29871	60239	A	30054	1	1986	
29872	60240	A	30055	339	596	PPYKRKRKRRESVSDGMRNTG KTRRTR*INLLGRS*NRNFVSV PSGQNPY*ISLDHGRENYGGYS TIQRLLRLPLSRSGCILQ
29873	60241	A	30056	634	924	
29874	60242	A	30057	42	665	KYGVNPGPYGGTTRKLYEKK LLKLREQGTESRSSTPLPTISSA ENTRQNGSSSDRYSDNEEDSK IELKLEKREPLKGRAKTPVTLK QRRVEHNQSYSQAGITETWTS GSSKGGPLQALTRETRGSRRT PRKRVETSEHRIDGPIVESTPI AETIMASSNESLVNVRVTGNFK HASPLPITEFSDIPRAPKKPLT RAEVG
29875	60243	A	30058	1822	4791	
29876	60244	A	30059	310	1275	
29877	60245	A	30060	52	390	
29878	60246	A	30061	250	1530	
29879	60247	A	30062	1	1641	
29880	60248	A	30063	1009	1140	
29881	60249	A	30064	913	1218	
29882	60250	A	30065	900	999	
29883	60251	A	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	A	30068	1	2229	
29886	60254	A	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSCFVWKTAWAQKMN LLPMARLTTTIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALLTVTT QATGLRLARQKRTATPRTIRPG ESTSSPRSSGSLAPACSPVWM

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29888	60256	A	30071	498	1155	KQPSAVSGTGAAGEANLHAVR TAEQTAVVYRHRQVRVYLLR YGILDWSPITYLKEVKHFDKDS SWAYFLYEYAGIPGTLLCGWM SDKVFRGNRGATGVFFMTLVTI ATIVYWMNPAGNPTVDMICMI VIGFLIYGPVMLIGLHALELAPK KAAGTAAGFTGLFGYLGGSVA ASAIVGYTVDFFGWDVGFMLS HELWESEFTKLKYEYNNSCPAS VSGWL
29889	60257	A	30072	670	1100	NCRKTSPKRRFSDDPKSDRAK DFLAKILH*SLWRAPYPIARHLTL YRFAPRICYILALPLSQSRSTQQG ATMALPILLDCDPGHDDAIAIV LALASPELDVKAITSSAGNQTP EKLTLRNVLRLTLNRTDIPVA GGRGKTVNA
29890	60258	B	30073	861	955	
29891	60259	A	30074	1	2510	
29892	60260	A	30075	3	119	NALRKSSASSCSGRNRYPGS*PS RPDCQRCSCSHKHAGYG
29893	60261	A	30076	3	227	GGEGRASCADTGWLPSPDPPGC AAGALGGGGWAVAGAAAGGP CA*SAGGIGVHAPKAQHPATFS GPAEGVIPPQ
29894	60262	A	30077	1	2277	
29895	60263	A	30078	1	2187	
29896	60264	A	30079	1	3666	
29897	60265	A	30080	1	699	
29898	60266	A	30081	513	1019	TGGVCCWCARYVDALVVFAD QLFVAEVLASAHSPRLYAHAAH GDTQPQLRLNLRGQALSP*FCCN HRAALQRHQFVRPLPAROSRO MRRCNLLYQKASQRSQRDSS *RSLFFRSVDADGG*R*SHGYA FRHGRFQCHRPGLPGTGPPRH ADSAFSRRLIYPACRWRL
29899	60267	A	30082	389	462	
29900	60268	A	30083	1	278	MGVNDAVLEMHGLGNDFMVV DAGFDQLLVVEPPYDLELDFHY RMFNADGS/DSGAVRQRCALLC PFCASERTDQ*A*YPRQHRQRA DGSDRHR
29901	60269	A	30084	1240	4914	
29902	60270	A	30085	1	1308	
29903	60271	A	30086	30	164	VTWW*RAPTAGLMQC*YCRNR RARLRLTYGHAPHRNRGPDV PS

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29904	60272	A	30087	3	264	TLRPANRF*HIPDAAGVIPVGY AL*RGTSVSVAHVRW/CSIVFGV NWATLAKTLMVAGIRRSGAAS RISRASPPSFSVPACSVGRKKVI
29905	60273	A	30088	1	3639	
29906	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLLV FADCLAWTCRHDKLDDISDVA KITGLTSKAIRFYEEKGLVTPPM RSENGYRTYTQQHLNELTLRQ ARQVGFNLEESGELVNLFPDQ RHSADVKKRRTLEKVAEIERHIE ELQSMRDQLLALANACPGLDSD ADCPHIEHNSGCCCHHRAGKYVG LIRRVKRRIRHRCWPIKTLQRA VSEFQRLIQPNHQYQSYTRQCA PETDNHADNSYNAGLFIVNSLY TAEGVMDKHSWQRYVPLMR HEALRLQVRLPASVELDDLQA GGIGLLNAVERYDALQGTAFITT YAVQIRIGAMLD
29907	60275	A	30090	1	699	
29908	60276	A	30091	430	660	HQTHFIVEHRRIMQRTARQNI RHYQQLSAVQIRIGAMLDLRL SRDWVPRSRNRNAREVAQAIGQ MSLPLMLQVALS
29909	60277	B	30092	1	1575	
29910	60278	A	30093	1	289	MISANRPIINLDDLRTFVAVA DLNTFAAAAAVCRQTQSAVSQ QMQRLEQPLGKNCSLVTVA TN C*LNMAFNFLVTPGKSCVLM M RSCIQPNSD
29911	60279	A	30094	1	1095	
29912	60280	A	30095	1037	1297	LILRCPSWSYRCIRILAPSS*Q TEAKPFASRASRTSDCQWANI SSVMPVKPNSTTSPILRRFSTPK CSATNCGEN*LSIMIGS
29913	60281	A	30096	905	2042	
29914	60282	A	30097	87	760	
29915	60283	A	30098	1	2793	
29916	60284	A	30099	308	485	KSLNAICYRNRTRTSMACY*PA* VRWPKHSAGLMTISPLVHVISP RHWRLCATRVGRGLG
29917	60285	A	30100	1	2784	
29918	60286	A	30101	453	1975	
29919	60287	A	30102	3	470	
29920	60288	A	30103	1447	1773	QFATFHHQTEHHHQRSYDC PQRDPRIHDAQVSDQRPDPDSG LREPLHCAQPDSSG*ADNSADH IRRNGGDGAFQKRNRNRLTDPH KRQEHGGLTLRIKLSVEQAFAG
29921	60289	A	30104	1	449	

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29922	60290	A	30105	188	1508	
29923	60291	A	30106	171	410	
29924	60292	A	30107	3080	3232	
29925	60293	A	30108	1	1272	
29926	60294	A	30109	438	617	
29927	60295	A	30110	259	392	
29928	60296	A	30111	905	1545	RLTTPSLSVCWRPAAKRPIPRSLKQLKKIASRKVTP*/SLGNAWNNLEKQRAYLSMMAQKRVDGGLVMCSEYPEPLLAMLEEYRHPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGLERNTGAGPPCRFYEGDGRSDDQVVDGIQFFFTNTITGRGHFRITMVDGICPCCKDGNLRFNRILEHREPFYQIPATFAYA
29929	60297	A	30112	3	466	AIVKFKRNVHQDGGYCSVQIQCRFALIFKDFCRMHRHGLIRRITISQQSVGRIRCVSIASGRVYYCFFALEGKKPSSSIAAPTQMAVSAARLKVAKCQSPT*KSIISTTKPCHRRSNRLPSAPPIISATRVHRQMRYSTSSGAALLSITVTPS
29930	60298	A	30113	1	1562	
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLLTSLLTSVV*IDAIDGIRFSLSWASGKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRRREREKTSERTAPV*VKITTRKLYPAERTGRIFEAF
29933	60301	A	30116	1	3095	MDKFLNTYTLPRLNREEVESLNRPVTSAGLEVIINSLPIKKSPPGDGFTAIFYQRYKEDAGEREGEGNQQVAVRGKRKTTERKKKLGEDVKVKESKNSGAYEVKQHRFRSLDWNLSLRQKAEIFIPLESEDDTSYFDTRSEKYHHMETEEEDDTNDEDFNVEIRQFSSCSHRFSKAAEVSTRLLSTRVTEIEGWLVQRNQKLLQSNLKQRSGEPLILDDSHVPPPELRAGYRLKNAGCLPPELEQRREAIQ
29934	60302	A	30117	1	2583	
29935	60303	A	30118	1	3141	

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29936	60304	A	30119	1	1037	MRVVILGSGVVGVASAWYLNQ AGHEVTVIDREPGAALSTAAAN AGQISPGV AAPPWAAPGVPLKAI KWMFORHAPLA VRLDGTQFQL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRA PDTLNTMPIFKA CTPDNRRAVWRHRAQTSPESR LLDMTAAWIEIANHHLQRFTTR LQQLGIKTNNLRHSGKTNAVIV YMIQSISLVDEMSCHLVLTGG TGPARRDVT PDATLAVADREM PGFGEQMRQISLHFVPTAILSRQ VGVIKQALILNLPGQPKSIKET LEGVKDA/EGVPYCIQLLEGPY VETAPEVVA AFRPKSARKDVSE
29937	60305	A	30120	96	711	
29938	60306	C	30121	128	628	
29939	60307	A	30122	1024	1128	
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHFV ATTNRLALSIWYLMN
29941	60309	C	30124	202	321	
29942	60310	C	30125	150	491	
29943	60311	A	30126	1163	1257	
29944	60312	A	30127	929	1023	
29945	60313	A	30128	3	765	TARAWLLGLPVWPCVSERWSK KPSPRGGRDPSDRDPAFAAARS TVPPRISAYERPVPWGEWNDP RGPGRRASAVVSPREGNWGVL RDPRLQARKPRMVRSRQMCNT NMSVPTDGA VTTSQIPASEQET LVRQESSEDYSQP*LLVALFIAA KKM*KSLGKGP KTKKRVWN LVCPLMPLNLV*FVKVLDKLV ALSMKQDILWPA LH/DAKKL KKRNKPCPVCRQ/HNSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	A	30129	2	430	
29947	60315	A	30130	3	1088	
29948	60316	A	30131	303	529	GTGQCANTKMSVPTDGA/VTTS QIPS/SPEQETRV R/PKPLL/LKLL KSVGAQKDTYYGKRFLFNLG QYIYGLNDYY
29949	60317	A	30132	3	619	
29950	60318	A	30133	123	385	

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29951	60319	A	30134	66	413	HQSEQMYQSSSECLLGTAKA RGHQLRTASACHFPSTPPFWSL TLESQREGRFKQPTLISCF/CLF MSVPVVSAPPFSSSSSSSSSS SRPWFDPQEAR*LTSPVERPCR GLRPA
29952	60320	A	30135	257	465	VPTSPASLESKQSCPHVLCVPW EVEGHVS*TGKPDPRPRRLLT LLLVPVWVPGQLAIKQEGQEPK KRH
29953	60321	A	30136	1564	1857	
29954	60322	A	30137	33	265	
29955	60323	A	30138	114	560	
29956	60324	B	30139	70	555	
29957	60325	A	30140	650	1045	
29958	60326	A	30141	374	575	
29959	60327	A	30142	1	1095	
29960	60328	A	30143	1	981	
29961	60329	A	30144	28	698	TACRIRHGHAGRLCCSPCLLVIP LKSSQHLRLVLPNPNLDGRRKI A/FAHHCFFKGVGRRYA/HVVL RKAD/IDLTKEGGENSLEDEVE RVITH/LQNPRQYK/IDWFLN KTRRM*KDGTYSPPG*PIGLGQ QAPVKDLGAD*KKIRAH*/RGL RHFLGAFRVRGQAHQEPGR GRHPSGVSKEIRSVGPCLVNKI VYIPKKKKKKKVDAAANLVV VVVVVGG
29962	60330	A	30145	107	340	
29963	60331	A	30146	428	934	
29964	60332	A	30147	1	1533	
29965	60333	B	30148	1	2652	
29966	60334	A	30149	205	450	
29967	60335	A	30150	1	879	
29968	60336	A	30151	139	1029	
29969	60337	A	30152	237	422	WFETPAQYTNRSPESTGYHRR RSRARWHGCMCEVCRRRKS PRANKPRLLPPVR*RCPPRA
29970	60338	A	30153	1	1134	
29971	60339	A	30154	136	411	
29972	60340	A	30155	1	3345	
29973	60341	A	30156	194	475	TPATVRRGWRPAVRVFRWVK PLTVPPRRKGPLSRGTGCRPVPL TTPSTGTVMRAGICAVKMLIVQ KSPCMPPC*HRQWTMTGLWQA PAAIRPV
29974	60342	A	30157	1	2988	
29975	60343	C	30158	1	3939	
29976	60344	A	30159	308	749	
29977	60345	A	30160	1	1338	

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29978	60346	A	30161	1	4342	MTRDNPVIFRHRREVVFQGE NGGIQNARFIAALFFQHGYNLC QRVGGLLKGGVEVFRYTSVVE RVVVDYYIRPAGFSIDTNRGS VTDDFAPDQLAKAIPGFKPRE PQRQMAVAVTQAIEKGQPLVV EAGTGTGKTYAYLAPALRAKK KVIISTGSKALQDQLYSRDLPTV SKALKYIGNVALLKGRSNYLC LERLEQQALAGGDLVPQILSDV ILLRSWSNQTVDGDISTCVSVA EDSQAWPLVTSTND
29979	60347	A	30162	1	1023	
29980	60348	A	30163	1	679	MFRVTWSSGRTGLGKRLFRTP YDNDDTGYPYAFNKTHPKDNYT CTVLFIDDMASGQSLDKAQD NYRQAMKKLSSGRGNVLAQAE AFRGLGVEIKREINPDIAEQAIR LQDCVFDQTETMTTFTGTVSS ANSGYYTIFNTDTGAAFNNVS LAIGNYVVLAFSAS/VGA/DMK MVNSTITASGSKRSTTVLRQGL SQRWLLSAGARNLLQHYSFRE TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	A	30165	1	1353	

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29983	60351	A	30166	1	1661	MRGEVLLAGVPRHVAEREIATL AGSFSLEHQNIHNLPRDQGPNG TVSLEVESENITERFFVVGKRV SAEVVAAQLVKEVKRYLASTA AVGEYLADQLVLPALAGAGE FTVAHPSCHLLTNIAVVERFLP VRFSLIETDGVTRQLLGVSYRIL AMGHAEFLIQIADMRNDGGWR DFQFSGNLVMDPEPNRSQAITYIK LVKSRLGTTKRYNHKDDCPRC RWIAAMIDNPPRIKPTKSASV WHATATSASPERQMSTTVIMS ARFISCVWMTFCMPRSGPMRF VHLPCRFRDAFNTGVGKLQDL GPSMSTRIRQRFTTLCPMTLSSS STEFENVSDCRPSRARSCLRFRL CRSIRCYYRLADYVQRSLQAGF IQRPAIRHPYHHVKGAFFEYVR NNRLPETVIRVLQPALARFSPDI APLFSPPFLHDDVDTARLYAPS LMPKLRLIGLTLALSATAVSH AEETRYVSDELNTWVRSRSGPD HYRLVGTVNAGEEVTLLQTDA NTNYAQVKDSSGRTAWI/HVET T*H*AKPALPCARSGKSGQNPD R*THQYR
29984	60352	A	30167	254	496	RASRLKTCGDGCCSLSAVVSVG ASPFASRVKSSRRVW*S*VGPSS WPPGMSL*TAEIRRSRRIPVSS GSLTASFANVVR
29985	60353	A	30168	1	984	
29986	60354	A	30169	1	429	
29987	60355	A	30170	1	523	
29988	60356	A	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	671	
29992	60360	C	30175	1	2649	
29993	60361	A	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	A	30178	3	108	

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29996	60364	A	30179	404	1347	DVTILARA VLQALLKILYH/KCE FNDEMLTEGVIREKMGFNPQTL REVLQACQQQGCVANL DLDV VMIIIDGAFSGIVQNWL MNMA GYDLYKQAPALVDNRTGMER ASNGGPWQVQSLPARSYRQLD SYYGEAMAIGERALVALLDFSG PSPSGDWRYQTHHTFPPTGWR RQATLVKMRACIEAVKAVGEE LCPALGLTIPVGKDSMSMKTR WQEGNEEREMTSPLSLVISAFA RVEDVRHTITPQLSTEDNALLLI DLGKGNNALGATALAQVYRQL GDKPADVRDVAQLKGFYDAIQ ALVAQRKLLAYHDLRI
29997	60365	A	30180	494	1433	
29998	60366	A	30181	1092	1347	
29999	60367	A	30182	315	600	STPIEKTVS KAFSAGSCSILTVT NARASARSACIISITA AVSGSCA PTP*EVSSAFARSLICRSIRKPGL KLRSITIGALASKTVP LPA SPPIA
30000	60368	A	30183	535	661	
30001	60369	A	30184	1	1491	
30002	60370	A	30185	1400	1852	
30003	60371	A	30186	199	534	
30004	60372	A	30187	2	539	
30005	60373	A	30188	1	690	
30006	60374	A	30189	127	939	
30007	60375	A	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLC LTDERTRRNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERS DEIPEAAKEIMREMGINPETWE Y
30009	60377	A	30192	242	709	NYMHYHADRCITRCHGNACTV NYAGLSVPSTVW TGLNLLT KRIKYLMAEWSGE/YISGPCVEP GKKSQSKKITVSIPLKVLKILT DERTRRQVNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERT AEIPEAAKREHA*HGGLTPET WEY
30010	60378	A	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263	514	PAHFSVAHSHLWQNNPLSSVQ CRQNHQAIPCRIFELNVMRH/ VTRDSSSLGCSWRLTASVNR RFVDPVQILVMAMSGRRSR
30013	60381	A	30196	1	1995	
30014	60382	A	30197	141	229	

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30015	60383	A	30198	1	702	
30016	60384	A	30199	36	144	DGLLLMDERNISPLLQKRMT* QAV*VWWWKDYGV
30017	60385	A	30200	462	646	QWVPIARPMPACHVQRRTSSL ERRQPVMIMVMLRII.WYIYCSI HVLG*WICRLYYKTLK
30018	60386	A	30201	107	1200	
30019	60387	A	30202	366	500	
30020	60388	A	30203	1	1193	LADCSRYNGLEMTLSCCAGAS TDAVGGIERGGLKSPASEGEI APRLLLDGEPLALSGDKWRISP WLLVTDATITAFLOMIQEGK AITLRDGDQTISL.SGLKAALLFI DAQQKRVGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPTL SLEERNLLDYGNGWRMNGRLC SLDPLRREVNVTALTDKALM MISSQIFNGHMHIIKDLVFTDH APDKGISFGSDTGMDRPARGD HRLVMHHDMTFRFLR.PHHVE NAGVHHIEIEINFHPALVGVTRH GVPLVTRSQLRQPHTRLAGFY IRDQIFVNRATVTGEEIAYAEF TNFPANGNRFYSRHNAANNNS VNVAVNHGVLIGDKYLFNQKFI AQPLGIQRFVVRTVDALSYVHI
30021	60389	A	30204	3	1057	
30022	60390	A	30205	1	955	
30023	60391	A	30206	1281	1370	
30024	60392	B	30207	1	2199	
30025	60393	A	30208	1	589	MLKKREQTVFTEHESVFQGLD RGNRELGPPTFGVKGAQKGN LQIFSEDKNFGPGSGEIVGHR GPKWDIPRGKRETLGKPHFFW KPSQEFGRKGLSGFSPWERVSG NKNSGKRIYPWGPVDGINCRW REPRNVDAEYRRDCGSRFRSL RHFYRSLFSLHHPASTRHQKAQ SSAVTVLQTNAQHGRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRTCAPLSSVWRCR PPRSSPWPASWRSPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCL.WTSSLAPASRP CPS*LQPPGQQRWGEPIGAIAV PL

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30027	60395	A	30210	61	641	RHKHRRRIPGRWDQIRPAPNR WQTGFQWFALPVTGVRLISGY TELLPRL/PAQKNLPYTHPAWR FVAHQGRESALECRYVPLPVRH *RNCRWREPRNVDAEYRRDC GSRFRSLRHFYRSLFSLHRPAST RHPGAQTGAVTGFADECPARK AAALAKASVNVVFHSTNATV CHRPDRSRASGSFRYYWRQE
30028	60396	A	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLSANSKNRR WRKNIKLR*SSLLK*TESPLPMA ILVLTSLTAI
30030	60398	A	30213	451	834	IWTGKKVDSARALIARGWGLH VILRRTDWMDGRRSRHTDDT DVLRLHHVIGELPTYGYRRVW ASSQTGR*FKVQNRYPFPVLS DFEHLQEPYEFGLR*PWLPA TGEFHAIEYRSVDFCKHPV
30031	60399	A	30214	1180	2547	
30032	60400	A	30215	341	505	
30033	60401	A	30216	293	4221	KPFSPPCKRGRWLFNRHSSARR PTVLYYRRSTMR*NSW*PNLRR QRGNPANRS/RQSMLELSGVKD GELIPAKLFNLVTWLQARQTL SQQNTPRPGGGEIPWCCSVLA ESERKKRGRKKQRGIDSPDVGA LLLVRATFYIWQQPPVNKIALGI EYAAASKYYGWQRQNEVRSVQ EKLEKALSQVANEPITVFCAGR TDAGVHGTGQVVHFETTALRK DAAWTLGVNANLPGDIAVRW VKTVPPDDFHARFSATAR
30034	60402	A	30217	1	1362	
30035	60403	A	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWRR*SP QYARHTRKRTSAGCSA
30037	60405	A	30220	1160	2385	
30038	60406	A	30221	290	373	
30039	60407	A	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	A	30224	1	469	
30042	60410	A	30225	241	615	
30043	60411	A	30226	1	1428	

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30044	60412	A	30227	862	1453	SFLLVSPSQACHHYAP/KIFDL/SGYTSTTEQMWGTVIVGLTNV/LATFIAIGLVDRGLGFLAMPAGM/GVLGTMHIIIGIHSPSAQYFAIA/MLLMFIVGFAMSAGPLI/WVLCS/EIQLKGRDFGITCSTATNWIAN/MIVGATFLTMTNLGNANTFW/VYAALNVLFILLTLWLVPETKH/VSLEHL/ERNLMKGRKLREIGAH/D
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCPPVS/VHFFHSRLCRDALNEAFHPSG/FQVVKCCDIARIHRNRYGDLF/AIGVVHIANVNIAHRNATFHQR/QEIGGCFTNQDFLSIGGAMNV/VDNFLQRPETYGDPFCQYHFH/QVLLYRIFGNLVGYQHQCIPR/KSDPLNADLTVNQAFINPA*NN/IWHSVFLFVLLIGLHRLCGMRQ/DVLNMVDNEFPWRWLQLAGA/NFHVLQRQILADQQRQNW
30047	60415	A	30230	2553	3845	
30048	60416	A	30231	1	656	
30049	60417	A	30232	3	228	
30050	60418	A	30233	185	206	ATVDPPFITEPGDILAGGFA*PL/SWFAGFALEHNLPLWATGDLH/SLRA
30051	60419	A	30234	12	155	
30052	60420	A	30235	698	2684	
30053	60421	A	30236	1	2004	
30054	60422	A	30237	1	811	
30055	60423	B	30238	1	7521	
30056	60424	B	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPWNRRKPVLSVIP*K/WKLKGPVALKTAYPKRLPLPI/TSFSLPGVA
30058	60426	A	30241	1	2067	
30059	60427	B	30242	1	2787	
30060	60428	A	30243	101	947	
30061	60429	A	30244	1	1917	
30062	60430	A	30245	239	469	KRVSISSRRRFSAQKASASALA/RWWRSAVNIIYVFAL*TTAQRV*QLRMTNCVRTTITACHSR*RTLL/SLSPVKPAS
30063	60431	A	30246	1	4348	
30064	60432	A	30247	1141	2244	
30065	60433	A	30248	503	649	

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30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRFLFIGAERFQHIAGSGHYR VV*NANAGSKIIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNPFNFEIFQRLVDDDP HCTIGIMFANVDHGTGTENRIRK LCFNLTNTGTQKKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	A	30250	1	526	
30068	60436	A	30251	442	684	
30069	60437	A	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPPLPTENVP AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDPRLAIRDATIGISG FCSLA
30071	60439	A	30254	62	298	
30072	60440	A	30255	904	1530	
30073	60441	A	30256	701	1329	HRLSMCRGRCRWSWARTNVI SMLVFALSFASWRIVSPRTM/D ALTFAAESALPGSPTHISTDHQG QFVFGVGSYNAGNVSVTRLEDG LTMHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTPPEA CTTNKQPAQQRDKPQRGNQ RLASVIFQCQHDHEHKEHRTY PAHQLAERHLVDRLLM
30074	60442	A	30257	8	382	
30075	60443	B	30258	1	2655	
30076	60444	A	30259	67	231	
30077	60445	A	30260	1109	1531	TFLHSIPAAKTQGPPTNTLVDT PQHL*HQQRRTQPOLALSLRT *VFLNRLRGALFAPKACLPD LVISPRGPPQGLGVTRVQVSAH TNPTRTTHRNTPHYTRNTQTRPE STPRRDITTPQQRHTPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDSDSPISQSKMKIIA SITTIRMEP*AIATPYSPSSTRLM M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSDSPISQSKMKIIASITTIRMEP *AIATPYSPSSTRLM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	A	30263	3026	3217	LPQCKWDPYGVGTISPQVSIISR ANPCTSPFFV*SATKGLLYQQ TRIPALDIPSSNRRNSHG

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30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPYHGRWPQ HDFPPFKKLRPQSVTSRIQPGSD VIVCAEMDEQWGVYVGAQSRQ RWLFYAYDSLRTTVVAHVFG RSLFTGP*RRERFATQIEVGKLF AAVDMVLWLSGKAQPDVVV KVVVL
30082	60450	A	30265	3174	4135	
30083	60451	A	30266	1	2771	
30084	60452	A	30267	1	1281	
30085	60453	A	30268	10	233	LRIQASDPEINSRRESGHIPLPYT DKAPSLTVDGAK*EVSRSR/R QNSQVQHPPDAAKYPSGCHK FRGFRRA
30086	60454	A	30269	300	564	SANSTLKRQTQVNRRLTVKLSA RKLPLMKVNTNRSLVVVSMV MLLSTCTRWSRVQTRKATSSST TLKVV*SLANTSRPLIKVSRNS
30087	60455	A	30270	5259	8003	
30088	60456	A	30271	1	819	
30089	60457	A	30272	1173	1369	
30090	60458	A	30273	1	4767	
30091	60459	A	30274	905	1162	FSSVVMCSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSRCS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	A	30275	1164	1582	
30093	60461	A	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGV RLYAANQHRTCC
30095	60463	B	30278	1	954	
30096	60464	A	30279	108	530	SIRQTHVQIVRRSCLAIRHQVPS TAIRVGIVKGNFAS*AGAQP SLR*HRCCTRALTSGLVAVRLS AGCNFPELVHRRLLTWRAGR TYPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLT PFPAGQRC
30097	60465	A	30280	1	1389	
30098	60466	A	30281	1	380	
30099	60467	A	30282	1	3255	
30100	60468	A	30283	569	2547	
30101	60469	A	30284	1	585	
30102	60470	A	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGS LGPSSGPKTAGAPSSRPSPSARR RTTETRWTLRLSKDYWLITRK VGLGNLQDGGGRAGSL

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30103	60471	A	30286	737	1088	NMLMNVNLPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRLPIIVGR RKSGGSKIRANVCSLPIFPGIG R*TTGESKRICRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPFSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAESTSPLAMVGD GINDAPAMKAAAIGIAMSGGT DVALETADAALTNHLRGLVQ MIELARATHANIRQINITALGLK GIFLVTTLLGMTGLWLAVLAD TGATVL
30106	60474	A	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPF IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFIIVGTSGLFNHAENIDEAW RVMTAQILAAKSEQWGQQVY AIVQNTDQAQAVMPYGPCKLY VLAQNDAALQRTENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTNASLAGIALNSMDLSP GGRVAVKESNQRCWSDGFEFC CDNGERLVRVTFALDCCDREAL HWAVTTGGFNSQTVQDVMLG AVETPLRQRSSVVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQRSIRHPAPALRYPQLQ MPHWRRSICTSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIKASLS*FK*LLKPAINAG*Q AS*WRASASKPCASPDACAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	A	30294	1246	1300	
30112	60480	C	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCQVD
30114	60482	B	30297	1	3081	
30115	60483	A	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVA TKLRR *RVFPAPCCG

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30116	60484	A	30299	3	421	QRRATGDLRLPTR*TARRGGRCDS*SSRRWHRAFTGACREISRQ QNRHRQRPAAGVALVGSE*Y SGILAGQRHYRVYRAGYRRSP AGYAPD*SD*RPVDGRHECGRR PVWRRENVPTAGGQIGARHET GGGLPRTVY
30117	60485	A	30300	1	3202	
30118	60486	A	30301	317	554	
30119	60487	A	30302	474	599	TTSVQRTFLPDITY*APTPVLLPA RKATAARKLHRFSGRQDR
30120	60488	A	30303	212	569	TSKVVTPALRSMPSVPINNLS KVKCSKAFAASCP*NEADFLRN VPPGIRIVCSLSSSDSALTICRL VITVMLLKRESRGITICKTVLPAS RMIESPSWIKLTAASAISSFLWV LMSVL
30121	60489	A	30304	1	160	WSKMSRAVRPSDWESWTQTRE VVRQTVRCRDPPSAAVCLTAS SPANCGIPIG**MLAEILA*RAV RPSDWESWTQREVVRQTVRC RPDPPSAAVCLTASSPANCGIPI G
30122	60490	A	30305	1	975	
30123	60491	A	30306	1	762	
30124	60492	A	30307	1	733	
30125	60493	A	30308	493	948	LGAIFLAGALFAAAWLADFRL GLGARLYRYGADWFCADGGM SAEELKFISENGAVVMDHKKP GSAAASGPKLHYIKQLLSNRM MLGVFFGQYFINTITWFFLTWF PIYIGNVVSDNR*YVAQITITW IKTYGRCPSFQRDGDGFVNRCL

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30126	60494	A	30309	153	2031	RRNYQRQKKRGSEGAGRDPDR RSRISAAYSRSEFNNAAVTEH Y*NRFT/LVPRSR/HANADTVT REAVNQVIALLDGSGALRVAEKI DGLPTNQMQASRRAKEEEVHL TGQPSRVQSPRRCEEKQYMVLL MIVSGRSGSGKSVALLRALED GFYCVNDLNPVLLPDLARTLA DREISAAVSIDVRNMPESPEIFE QAMSNLPDAFSPQLLLFLDADR TLIRRYSDTRRLHPLSSKNLSLE SAIDKESDLEPLHGFDPDYDTV GFSCRRRIDYVCRHKHSRRIRQV VLLNFAKSGAFSTTRGDDKTR RSLLVTLVRIFCVRVIFAYDIRD GIHVRRIQINSKSGKVGSKHNSG YSAAKFGGVGLTQSLALDLAE YGITVHSLMLGNLLKSPMFQSL LPQYATKLGKIPDQVEQYIDK VPFKRGCDYQDVNLMLFYAS PKAVVLAPDSRSMSPAVSGRFK PRVVVAIALDDQQRIVDTLFMK GLTVFARQKIPAITGRHSGATL QKQKCSVEELAQYFDTTGTT MRKDLVILEHAGTVIRTSGGVV PDSPPHTRRDPRRFSMAFPWF NIRSAEFHHVTTLLAEIPRQOND IHRPAHAAAAPKVETRSGDET NRWNRPAQHLFA
30127	60495	A	30310	720	872	EKVPVSGPGGMQELPMQSPDR RSAGKPGPASRAGR*TGGAFA TKRDYR
30128	60496	A	30311	1967	2452	SRRCASINQRPBGHEKMMVSV RIAPASNVPTCRPITVTGSLAR SAWTHITRMVSPPLARAVRM* SPSTSSIEERVIRMTASGIVPST MAGKIIWATASIKLPSSQMAV SISIKPVNGLESSRNTISLTRPET GVRFCQTETSMISIMPHQKIGIE
30129	60497	A	30312	1912	3960	
30130	60498	A	30313	2	250	LIRKYST*VLMKAFLRIA*KDC ERLGLKCFWSGSEKGCPLVNT NAGGHCEHHQWVSSVSRV SQSAGGCLFNILLNTV
30131	60499	A	30314	1	300	SVFSH*AKKIWKGVSRALGQ NSRSGSGSCQASWTRFPVGFH TDGTRLRNPNMGQAFGLPVAR FLALEARSLDCAFSSLLFKRKL SGRWGRASRGTKL

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30132	60500	A	30315	1	468	MTEKVKQPPAPVTASDEIDIGR LVGTVEARWWVIGITTVFALC AVVYTFATPIYSADALVQIEQ NSGNSLVQDIGSALANKPPASD AEIQLIRSLVLGKTVDDLDDI AVSKNTFPIFGAGWDRMLMGRQ NETRRGFSARGTGQMLKKEGV TLMVEAIHASPGEFTVTKYST LGMINQLHNSLTVTENKDGAG VLSLTYTGEDRYTNHAGV VNT MIIIAATHNLVFENNSC EYAHF MGNAPAGL TEYQNVFYKHIDRI QGHYVWEWRDHGIAQDDHG NVWYKFGGDYGDYPNNYNFC LDGLIYSDQTPGPGKKEYKQVI APVKIHARDLTRGELKVENKL WFTTLD DYT LHA EVRAEGETL ATQQIKLRDVA PNSEAPLQITLP QLDAREAFNLITVTKDSRTRY S EAGHPATYQFPLKENTAQPV P FAPNNARPLTLEDDRLSCTVRG YNFAITFSKMSGKPTSQVNGE SLLTREPKINFFKPMIDNHKQ EY EGLWQPNHLQIMQEHLRDFAV EQSDGEVLIISRTVKPRGP ARCP DSSVGTITYCTENNPPFDNGLLN AQLLQQA KPFVDERQSK*FGCH SPSYSLWLSIIGLKKLIFGSRVS SDSPFTCQDVGLPLIFEKVI AKL
30133	60501	A	30316	1	524	
30134	60502	A	30317	1669	4421	
30135	60503	A	30318	2	349	SMAKCLPKRNQGPVRS CGAWS GCLWLPSPSGTPWRSSLWILL F/SQISQLLSLLHQGFQPKPNH RGNKYLAKPGGSRSAIPD TDGP SARAGGQTDPEQEGLDPEED LSVKQLL
30136	60504	B	30319	217	368	
30137	60505	A	30320	1	951	
30138	60506	C	30321	1	3729	
30139	60507	A	30323	1	2437	

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30140	60508	A	30324	1005	1815	PDLHCQKKHPTLCSGYWPFTRT PVHYAAFS*/HALGHLAFS/EA SLHSHRGQTALTTQKKSPAKSP TAATTETRVMRKISHGTRDPPG FASLMQ*MHYGKLCFAQSELL FQSLQRSHWTQSWWLCWPHW RLCWTQNWQWCPHWLTLCW TQSWWLCWPHWRSCWTQRW WLCWPHWTLCTQSWWLCW SHWRSCWTQSWWLCWPHWRL CWTQSWWLCWPHWRSCWTQS WWLCWPHWRLCWSQSWWLC WPHWRLYWTQSWWLCWPHW RVCWTQN
30141	60509	A	30325	2436	3678	KMPWPFGSPGLGCSAWAEA PPAHCPCDVLHLHPACPHIQAP CGTGAPGTGLAAAADESEPLGSS APPAGRPCQAAAACGLAPPLP RGWCPPPTSSWMGRRQLQSLA HPTSPAPLLAAPTAVCSCSRCSA PRSRCVARPAARTGLPTAPAS SPAPATSPAPAESPAATASHPV AEASPAPGAPPRPAASPSAAS PAPPAASPVLTASPLPAASPAL AASPVHTASPPVHVASPPVHTA SPPVHTASPPVHVASPPVHVAS PPVSCSGDSTSDCFPPQGAFFP HSL/VSLRWLVSSCSCSTLDGP AGGCGARGSAVWFLSNKLLP/ MLLYQMYLMLLLLLRCANQ*I DVFSELDYCGA*IQGYC*FLV LAIPR*VVTRSGCVRATAIDFL FPVSSCWNAALPLPICF
30142	60510	A	30326	929	2910	
30143	60511	A	30327	1	1488	
30144	60512	A	30328	203	701	
30145	60513	A	30329	493	924	SDPGRFHGKARITDPRGQPGRR LQGGSENGSDMKAARKVSG NKHSTSSHQHAVWCPGVPS*SG KAWAADQRFVPRILGKGRGHV DAA*LSWKCRNHLSSVSLNGE NQRFVGDARYRTRLQGSANL FKRQRCGLHQNLELL
30146	60514	A	30330	1	2193	
30147	60515	A	30331	1	2990	
30148	60516	A	30332	2512	2560	FALRYRQPVRRHW*FHLVQRH GRFSRASGATWPASAAFAWP LLVCAPLSAASAAAPLRL
30149	60517	A	30333	1	2820	
30150	60518	C	30334	194	418	
30151	60519	A	30335	25	458	

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30152	60520	A	30336	860	1209	IPGNCRDSSGVGKERETNAGS QHHM/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPEPVYEKKPK KEVKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	A	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	A	30339	1723	1845	
30156	60524	A	30340	6	983	RRWACRSLSSSGRRSLIRRMGF VKVVKNKAYFKRYQVFRRRR EGKTDYYARKRLVIQDKNKYN TPKYRMIVRVTRNDICQIAYA RIEGDMIVCATYAHLEPKYGV KVGLTNYAAAYCTGLLLARRF LNNRFGIMDKIYEGQVELTGDE YNNESIDGQPGAFICYLDAGLA RTTTGNKVFGLKGAVDGGLS YPLTVPKRFPWF/DD5*KPRNLI AEVHRKPPHPWAQNVARLHAPT LMEEDIEDAIYKQFVRQYVKN SVTPDMMEEMYYKKAHAALRE ESSSMEKKAQGGKFKKKRWNR PKMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	B	30341	1	2043	
30158	60526	A	30342	390	1180	
30159	60527	A	30343	2	649	
30160	60528	A	30344	1	1929	
30161	60529	A	30345	1	773	
30162	60530	A	30346	3	484	NSSCRDPGY/CPIIVSLNSS*GSL LQDMPGPSKVISIILATRGAVNI TTVAYKSAVILSFTTASAVLSL RNVIGPLFASQPSFTIHFLFSHN GSAPLNAPDMANCFGLTALTSS LDERLFRNSAGSCCGIRNCFIS TLPPNTSTLTSVNSKGS5SVHG
30163	60531	B	30347	1	2775	
30164	60532	A	30348	1	1386	
30165	60533	A	30349	439	555	
30166	60534	A	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITRCRTK/ EQRYALSQAKSIADLMTGCTN FAFGKPGTGKNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMR5VGMILNLNY EAMKTLGERIMDRMTMNGG RW
30168	60536	A	30352	1	786	
30169	60537	A	30353	1	288	
30170	60538	A	30354	711	953	

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30171	60539	C	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	A	30357	1	420	
30174	60542	A	30358	1115	1561	
30175	60543	B	30359	501	555	
30176	60544	A	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	A	30361	386	1647	
30178	60546	A	30362	1	1179	
30179	60547	A	30363	1	1215	
30180	60548	A	30364	1282	1657	
30181	60549	A	30365	388	804	
30182	60550	A	30366	1328	1978	
30183	60551	A	30367	455	1000	
30184	60552	A	30368	291	303	RVRRRMMYTVTLYSFSANKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSQLTVSLL LLSFALDPSSTMLTTEESVE
30185	60553	A	30369	284	433	RVRRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	A	30370	290	425	RVRRRMMYTVTLSSFSANKNTY I*E*E*GLGWRHHIFLG*IQHFNR
30187	60555	A	30371	842	905	
30188	60556	A	30372	784	3453	
30189	60557	A	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSGSLGP RGGRGGCILRPSRGGGRGHGPT KAGPWPSPESRGR*DWKARGPP APSRGSPSRARARRGSGGGGPA DEPLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	A	30375	1	340	
30192	60560	A	30376	2	3336	
30193	60561	A	30377	22	419	
30194	60562	A	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECSWLF*SH MHVLLPRNRKEKLEIFRTQTY DVNAYKASAHNRSGPG
30196	60564	C	30380	169	415	
30197	60565	A	30381	3	1324	
30198	60566	A	30382	2	3455	
30199	60567	A	30383	85	2695	
30200	60568	A	30384	69	303	
30201	60569	A	30385	1	951	
30202	60570	A	30386	1	4749	
30203	60571	A	30387	176	1553	

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30204	60572	A	30388	1	425	MDQHSFLGFRPDHVAYDIRSLRN KANPDDTFEAQLFYGDIAIVK TSHLVKIDYPKFIVHGGKGSFIK YGIDQQETSLKANIMPGEFGFA ADDSVGVELEVNDGVTVREE MKPEMGDYG/PR/L*CVVSNHHP RCAKL RQGI
30205	60573	A	30389	3	1890	PSQPLLWFAGRPGRDGTGCPRC KQNSTCIAAVKMEGPLSVFGDR STGETIRSQNDKESFNEQKTCRI *RKRLV*LYEVAEHEIVMAAAS IANIVKSSSLGPGVGLDKMLVDDI GDVTITNDGATILKLLVEHPA AKVLCELADLQDKEVGDGTTS VVIIAAELLKNADLVKQEIHPPT SVISGYRLA/CKEA VR/YINENP NLLTQDELGRDCLINAAKTSMS S/QHIGINGDFFANMVVDVLA KYTDIRGQPRYPVNSVNILKAH GRSQMESMLISGYALNCVVGS QGMKPRIVNAKICLDFSLQKT KMKLG VQV/VITDPEKLDQIRQR ESDITKERIQKILATGANVILTT GGIDDMCKLYFVEAGAMAVRR VLKRDLKRIAKASGATILSTLA NLEGEETFEAAMLGQA/EEVVQ ERICDDELILIKSTKA/RTSASIIS RVPIDSMCDemersLHDALCV VK/RVLESK/SV/PR/GGA VEEA LSIYLENYA/TSMSGREQLAIAR VCKITLWLPNTLSS*CLPRDST DLVLQNLRAFVHNEAQV/NPER KNLKWIGLDLSNGTPRDNKQA GVFEPTIVKVRGLNFATEAAIT LRIDDLIKLHPESKDDKH/G/GS YEDAVHSGALND
30206	60574	B	30390	1	975	
30207	60575	B	30391	1	2577	
30208	60576	B	30392	1	3126	
30209	60577	B	30393	1	1134	
30210	60578	B	30394	1	2082	
30211	60579	B	30395	1	915	
30212	60580	B	30396	1	2658	
30213	60581	B	30397	1	2412	
30214	60582	B	30398	1	2454	
30215	60583	B	30399	89	2533	
30216	60584	B	30400	1	4083	
30217	60585	B	30401	1	1725	
30218	60586	C	30402	127	345	
30219	60587	A	30403	1	597	

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30220	60588	A	30404	3	3386	MPATASAGVPATVSEKQEFYQ LLKNLNPSCMVRQRQAEIYENI PGLCKTTFLDAVRNRRAGYE VRQMAAALLRRLSSGFEEVYP NLPADVQRDVKIELILAVKLET HASMRKKLCDIFAVLARNLID EDGTNHWPEGLKFLIDSIYSTN VALWEVALHVFWHFPGIFGTQ ERHDLDIKRLLDQCIQDQDHP AIKTLARAAAAFVLANNENIA LFKDFADLLPGILQAVNDSYQ DDDSVLESLEIADT
30221	60589	A	30405	1	1695	
30222	60590	A	30406	1126	1355	
30223	60591	A	30407	1	1610	MGSRLNPPPPAHSDDTTGKDSF GNIRGAETGGASACSVTSARV TCGAGSEPHSHRNPISAQVGL APSYGAARGRRRPLALQQSPQE RRHVGNSTRGLLPASLPGTAS SQSASATASAAALPLKVTGPLAR NPTPPWTAALATRGQRPEK GLFPGPAPFSLGKRKRGRGRTW ERRRRVSIETSTCFRPGCERLGA AAGANLSQLASSQRPLRERWV LYTIIMAAAGAPDGMEEPGMD TEAETVATEAPARPVNCLAEA AAGAAAEDSGAARGSLQPAPA QPPGDPAAQASVSNGEDAGGG AGRELVDLKIIWNKTKHDVKFP LDSTGSELKQKIHISITGLPPAMQ KVMYKGLVPEDKTLREIKVTS GAKIMVVGSTINDVLAVNTPK DAAQQDAAKAEENKKEPLCRQK QHRKVLDKGKPEDVMPSVKGA QERLPTVPLSGMYNKSQGGKVR LTFKLEQDQLWIGTKERTEKLP MGSIK\NVV\SDPIEGHEDYHN DGRFQLAPTEA\SYVWVWVP TQYVDAIK\DTVLGKWQYF
30224	60592	A	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP SAAGRRAMKKKLVLCLLAVV LVLVIVGLCLW/LPSASKEPDN HVYTRATVAADAKQCSEIGRK\ AEVINAREVAPSVAFASMFNNS EQSQKAL
30225	60593	A	30409	562	2376	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
30226	60594	A	30410	604	2475	RQREVTRSPSPERSGLRVLQLFPP NPPVFRGQHPRLGPPSAAGR RAMKKKLVVLGLLAVVLVLVI VGLCLWLPSASKEPDNHVYTR AAVAADAKQCSKIGRDALRDG GSAVDAIAAALLCVGLMNAHS MGIGGGLFLTIYNSTTRKAEVIN AREVAPRLAFATMFNSSEQSQK GGLSVAVPGEIEGYELAHQRHG RLPWARLFQPSIQLARQGFPVG KGLAAALENKRTVIEQQPVLC VFCRDRKVLREGERLTLPLQAD TYETLAIEGAQAFYNGSLTAQI VKDQAAAGGIVTAEDLNNYRA ELIEHPLNISLGDVLYMPSAPL SGPVLALILNILKGYNFSRESVE SPEQKGLTYHRIVEAFRFAYAK RTLGDGPKFVDVTEASSGVSA VVRNMTSEFFAAQLRAQISDDT THPISYYKPEFYTPDDGGTAHL SVVAEDGSAVSAATSTINLYFGS KVRSPVSGILFNNEMDDFSSPSI TNEFGVPPSPANFIQPGKQLSS MCPTIMVGQDQVRMVVGAA GGTQITATALAIYINLWFGYD VKRAVEEPRLHNQLLPNVTTVE RNIDQAVTAALETRHHHTQIAS TFIAVVQAIVRTAGGWAAASDS RKGGEPAgy
30227	60595	A	30411	63	342	GRTLVPHGGLPHHYLVQCEWL PGTS*AEFPVVHLPAFVARARG ADRHGHGPFPLCHLHPARPRR EDLHRKSPGEPNIEHHRSSGPG CRRl
30228	60596	A	30412	1	910	MLFRPALGSRQVVRNMTSEFF AAQLRAQISDDTHPISYYKPEF YTPVDGGTAHLSVVAEDGSAV STTSTINLYFGSKVRSPVSEILFN DEMDDFSSPNITNEFGVPPSPAN FIQPGMGWR/KQPLSSMCPTIM VGQDQQVRMVVGAAAGGTQITT ATALICVTAFLPGRAPHAQPPS HADHTMPQAIYINLWFGYDV KRAVEEPRLHNQLLPNVTTVER NIDQAVTAALETRHHHTQIAST FIAVVQAIVHTAGGWAAASDS RKGGA YRILSALQEDKADKQS RDKILTRTRKGTLDGWLPm

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
30229	60597	A	30413	110	868	DLCLPLTPPHLLRPAIGSRQV VRNMTSEFFSAQLRAQISDDTT HPISYYKPEFYMPDDGGTAHLS VVAEDGS AVSATSTINLYFGSK VRSPVSGILLNMEMDDFSSTIT NELGVPPSPANFIQPGKQPLSS MCPTIMVGQDGGVVRMVVGA GGTQITMATALAIYQPSWFGY DVKRAVEEPRHLNQLPNVTT VERNIDQAVTAALETRHHHTQ IASTFIADVQAVIRTAGGWA SDSRKGGEPAGY
30230	60598	A	30414	1	1626	PSGREGCLIRESLKKILWLQAS AECEGDPGYFLSYFHQILLSFV ANTPRQGLGPPSAAGRRAMKK KLVLVGLLAVVLELVIVGLCL WLPSASKEPDNHVYTRAAVAA DANLCSKIGRDALRDGGSADV AAIAALLCVGLMNAHSMGIGG GLFLTIYNSTTRKAEVINAREV APRLAFATMFNSSEQSQKGGLS VAVPGEIRGYELAHQRHGRLP WARLFQPSIQLARQGFVVGKGL AAALENKRTVIEQQPVLCEVFC RDRKVLREGERLTLPQLADTYE TLAIEGAQAFYNGSLTAQIVKDI QAAGGIVTAEDLNRYRAELIEH PLNISLGDVLYMPSAPLSGPV LALAILNLKGYNFSRESVESPEQ KGLTYHRIVEVFRFAYAKRTL LGDPKFVDVTEASSGVSAIVVR NMTSEFFAAQLRAQISDDTTTHPI SYKPEFYTPDDGGTAHLSVV AEDGS AVSATSTINLYFGSKVR SPVSGILFNNEMDGLSSPSITN EFGAPPSPANFIQPGKQPLSSMC LTIMVGQDGGVVRMVVGAAGG TQITDTALAIYINLCFGYDVK RAVEEPRHLNKLPNVTTVERN IDQAVTAALETRHHHTQIASTFI ADVQAVIRTAGGWAASDRK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
30232	60600	A	30416	645	2571	GRPRLFPQLFPNPVFRGQHPR QGLGPPSAAGRRAKKKLVLVLL GLLAVVLVLVIVGLCLWLPSAS KEPDNHVYTRAAVAADAKQC SEIGRVLVGGPAYLLLLGKAEV INAREVAPRLAFASMFNSSEQS QKGGLSVAVPGEIRGYELAHQ RHGRLPWARLFQPSIQLARQGF PVGKGLAAVLENKRTVIEQQPV LWYVCGKVLREGERLTLPLRA DTYEMLAIEGAQAFYNGSLMA QIVKDIQAAGGIVTAEDLNYYR AELIEHPLNISLGDVLYMP RLSGPV/LALILNILKGYNFSRES VETPEQKGLTYHRIVEAFRFAY AKRTLLGDPKFVDVTENSIAGL LCARMDSPALGSRQVVRNMTS EFFAAQLRSQISDHTHTPISYYK PEFYTPDDGGTAHLSVVAEDGS AVSATSTINLYFGSKVCSVPVSGI LFNNEMDDFSS/PAFTNEFGAPP SPANFIQPGKQPLLMSCLTIMV GQDQGVVRMVGAAGGTQITTD TALPPSHADHTPMQAIHYNLW FGYDVKRAVEEPRLHNKLLPN VTTVERNIDQAVTAALETRHH HTQIASTFIAVVQAIVRTAGGW AAALDSRKVPTPGAGFWGLV EVGWWEAVITAQHLDIRGTG
30233	60601	A	30417	5	439	
30234	60602	A	30418	1	423	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,410,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30235	60603	A	30419	97	2012	WADEETWLCPLPHLPVFSPTAHL PLLSSPTFSSLLPFISTPHPRGFA LPLPPSARLYLELRKLPATLPWS SVTDGTGSLSGRRERGGEGERP GRRVRVADHGFALPRTGPOGS EEELANMQGLAVERLERAVSRL ESLSAESHRRPPGN/CGEVNGVI A/GVAPSRGKPLHKLMDSMVA EFLKNSRILSGDVELAEIVHS AFQAQRAFLLMASQYQQPHEN DVVAALLKP/ISEKIKETQFQRE /RTRGSNMFNHL SAVSE*1PCPL DGIAYSPKPG/PYVVKEMNDAA TFYTNRVLKD*KQSDLRHVDW VKSYLENIWSELQAYIKEHHTTG LTWE/SKTGPVASTVSAFVSLS SGAWGFP PPPPLPPG/PPSTFS EEWKGKKESSPSR/SALFAQL N/QGEKAITKGLRHVTDDQKT YKNPSLRAQGGQTQSPTKSHTP SPTSPKSYPSQKHAPVLELEGK KWRVVEYQEDRIDLVISETELKQ VAYIFKCEKSTQIKGKVNIIID NCKKLLGLVFDNVVGIVEVINSQ DIQIQVMG/RVPTISINKTEGCH IYLSSEDALDCEIVSAKSIWKWN ILYPPQGWVD/YREFPHF/EQF KTS/AWDGSKLITEP/AEIMALT SLRDRTSPSPESIKTNKKA AVK
30236	60604	B	30420	1	499	
30237	60605	B	30421	390	851	
30238	60606	B	30422	136	603	
30239	60607	B	30423	1	2190	
30240	60608	A	30424	82	242	
30241	60609	A	30425	1	330	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30242	60610	A	30426	215	1984	LLLVTMTSNNGLDIQDKPPAPP MRNTSTMIGAGSKDAGTLNHG SKPLPPNPEKKKKDRFYRSILP GDKTNKKKEKERPEISLPSDFE HTIHVGFDVAVTGFTGMPEQW ARLLQTSNITKSEQKKNPQAVL DVLEFYNSKKTSSNQKYMSTFS GDKSAHG YIAAHPSTKTASEP PLAPPVSEEEDEEEEDENEP PPVIAPRPEHTKSIYTRSVVESIA SPA VPNKEVTPPSAENANSSTL YRNTDRQRKKSKMTDEEILEKL RSIVSVGDPKKKYTRFEKIGQG PSGTVYTAMD VATGQVEVAIKQ MNLQQQPKKELIINEILVMREN KNPNIVNYLDSYLVGDELWVV MEYLAGGSLTDVVTETCMDEG QIAAVCRECLQALEFLHSNQVI HRDIKSDNILLGMDGSVKLTDF GFCAQITPEQSKLSTHG*GTPY WMAPEVVDTERAYGPK/VLDI WSLGIMAIEMIEGPPYLNENP LRALYLIATNGTPELQNPEKL/S AIFRWDFLNRCLEMDVEKRGFS/ SKELLQHQLKIGQAPSPSLTPH *LLQPKKATKEQSPKTHTHPQP HCAQAFCEINAHFRNSNS
30243	60611	A	30427	2	337	
30244	60612	A	30428	1	1644	
30245	60613	A	30429	1	330	
30246	60614	A	30430	169	440	
30247	60615	A	30431	1	1689	
30248	60616	A	30432	17	283	GHAWQLASIWLLCLLWPAVPL NCLSSYGWTLWWRIALVGA*R SLAPSRGSWSTQARPLKQRRTK WCGKSWCLSGTSEPLSHWPRL RSW
30249	60617	A	30433	16	346	RTDTYHLEDSKEQSGNRAGSG GWL*SCAE/GRRVALKSWPGRT GMSGTRRV TASSRGTSWYCGG SAGRSSTPTGRACSPGSFSSPE PQPPGPSAAGSSVSGQLGPCGG
30250	60618	A	30434	1	1772	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
30251	60619	A	30436	1	2607	MLTMSVTLSPRLSQDLDPMAT DASPMANMTPTVEQEGEEA MKDMDSDQYQKPPPLHTGAD WKIVLHLPEIETWLRMTSERVR DLTYSVQQSDSKHVDVHLVQ LKDICEDISDHVEQIHALLETEF SLKILSYSVNVIVDIHAVQILW HQLRVSVLVLRERILQGLQDAN GNYTRQTDILQAFSEETKEGRL DSLTEVDDSGQLTIKCSQNYLS LDCGITAFELSDYSPSEDLISGL GDMTSSQVKTKPFDWSYSEM EKEFPELIRSVGLLTVAADSIST NGSEAVTEESVQVSLSDVDKQ GCEEDNASAVEEQPGLTLGVSS SSGEALTNAAPSETVQQESS SSSHHDAKNQPPVCENATPKR TIRDCFNYNEDSPTQPTLPKRGL FLKEETFKNLKGNGGKRQMV DLKPEMSRSTPSLVDPDRSKL CLVLQSSYPNPSAASQSYECL HKVGNNGLENTVKFHIKEISS LGRINDCYKEKSRLLKPKHTSE EVPPCRTPKRGTSQKQAKNT KSSAVPNGELSYTSCAIEGPQT NSASTSSLEPCNQRSWNALQL QSETSSPAFTQSSSESVGSDNI MSPVPLLSKHKSKKGQASSPSH VTRNGEVVEAWYGSDEYLALP SHLKQTEVLALKLENLTKLLPQ KPRGETIQNIDDWELSEMNSDS EIPTYTHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	
30253	60621	B	30438	1	702	
30254	60622	B	30439	1	936	
30255	60623	B	30440	1	1494	
30256	60624	B	30441	1	921	
30257	60625	B	30442	1	3342	
30258	60626	B	30443	1	1072	
30259	60627	B	30444	1	3711	
30260	60628	B	30445	15	674	
30261	60629	B	30446	1	2127	
30262	60630	B	30447	1	3132	
30263	60631	B	30448	103	438	
30264	60632	B	30449	1	3042	
30265	60633	B	30450	1	1425	
30266	60634	B	30451	84	1954	
30267	60635	B	30452	1	1419	
30268	60636	B	30453	130	1615	
30269	60637	B	30454	1	1794	
30270	60638	B	30455	1	3255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30271	60639	B	30456	1	945	
30272	60640	B	30457	1	7437	
30273	60641	B	30458	1	1122	
30274	60642	B	30459	317	1630	
30275	60643	B	30460	1	1716	
30276	60644	B	30461	46	915	
30277	60645	B	30462	1	624	
30278	60646	B	30463	244	2988	
30279	60647	B	30464	1	804	
30280	60648	B	30465	1	1455	
30281	60649	B	30466	1	732	
30282	60650	B	30467	340	777	
30283	60651	B	30468	1	714	
30284	60652	B	30469	166	1337	
30285	60653	B	30470	72	617	
30286	60654	B	30471	1	1002	
30287	60655	B	30472	1	4173	
30288	60656	B	30473	1	4488	
30289	60657	B	30474	1	3822	
30290	60658	B	30475	1	1866	
30291	60659	B	30476	1	1002	
30292	60660	B	30477	1	1407	
30293	60661	B	30478	99	1046	
30294	60662	B	30479	122	1113	
30295	60663	B	30480	302	4145	
30296	60664	B	30481	1	669	
30297	60665	B	30482	1	933	
30298	60666	B	30483	1	2136	
30299	60667	B	30484	1	4017	
30300	60668	B	30485	1	1335	
30301	60669	B	30486	1	1095	
30302	60670	B	30487	1	2895	
30303	60671	B	30488	1	1215	
30304	60672	B	30489	1	2001	
30305	60673	B	30490	1	1281	
30306	60674	B	30491	1	780	
30307	60675	B	30492	1	858	
30308	60676	B	30493	1	699	
30309	60677	B	30494	1	1624	
30310	60678	B	30495	1	2958	
30311	60679	B	30496	30	658	
30312	60680	B	30497	1	1755	
30313	60681	B	30498	1	631	
30314	60682	B	30499	1	1528	
30315	60683	B	30500	1	1056	
30316	60684	B	30501	1	2305	
30317	60685	B	30502	1	723	
30318	60686	B	30503	1	2691	
30319	60687	B	30504	1	2322	
30320	60688	B	30505	401	2677	
30321	60689	B	30506	1	1218	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30322	60690	B	30507	1	906	
30323	60691	B	30508	1	2865	
30324	60692	B	30509	45	820	
30325	60693	B	30510	1	783	
30326	60694	C	30511	18	410	
30327	60695	B	30512	1	840	
30328	60696	B	30513	1	945	
30329	60697	B	30514	1	2108	
30330	60698	B	30515	1	2457	
30331	60699	B	30516	1	1156	
30332	60700	B	30517	43	4677	
30333	60701	B	30518	80	964	
30334	60702	B	30519	1	4521	
30335	60703	B	30520	1	2460	
30336	60704	B	30521	1	1854	
30337	60705	B	30522	1	1367	
30338	60706	B	30523	273	419	
30339	60707	B	30524	1	1786	
30340	60708	B	30525	1169	1443	
30341	60709	B	30526	1	486	
30342	60710	B	30527	13	1260	
30343	60711	B	30528	270	723	
30344	60712	B	30529	1	834	
30345	60713	B	30530	1	1632	
30346	60714	B	30531	1	4831	
30347	60715	B	30532	184	1593	
30348	60716	B	30533	1	615	
30349	60717	B	30534	1	3513	
30350	60718	B	30535	113	1666	
30351	60719	B	30536	101	2667	
30352	60720	B	30537	1	1692	
30353	60721	B	30538	51	142	
30354	60722	B	30539	1	3198	
30355	60723	B	30540	251	1207	
30356	60724	B	30541	1	1491	
30357	60725	B	30542	1	4024	
30358	60726	B	30543	1	3316	
30359	60727	B	30544	1	1342	
30360	60728	B	30545	91	810	
30361	60729	B	30546	17	489	
30362	60730	A	30547	1	504	MGGSNRSAAEWKLANGINIIV TSGRLLDHMQNTPGFMYNLQ CLVIDEADRLDVGFEELKQII KLLLTNRQTMLFSATQTQKVE DLARISLKKPE/LYVGDDDDNA NETVFGVTLCTDVAARGLDITE VDCIVQYDPPDPKPEYHVSGR TARGLNGRENWVFAT
30363	60731	A	30548	1	2676	
30364	60732	B	30549	1	1071	
30365	60733	A	30550	1	348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
30366	60734	A	30551	1	711	MAEIQHKTRIRPLEGRDLLAAV KTGSGKTLAVLIPAIELVVKLF MPRNGTGVILSPTRQLAMQTF GVLKELMTHHVHTYGLIIGGSN RSAEAQKLANGINIIVVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPCKEPLYVGVDEDKANATVD GLEQGHFVCPSEKRYLLFTFL KKNQKKKLMVFFSACMSVKYP YGLLYIDL/PVLAIHGKQKN KHTTTF*YCNADSGTLL
30367	60735	A	30552	661	987	VTFYSEHSNPNCHKNLKARRK DTKRIILKW*HTLV*GRDI*N*NI IITRNTYSLCPWATKKLKAC FISQK*KRDVIERNSAQCLQPKS IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	KFQGSNLTSETQNGDVSEET MGRKVKKKSKQKPMNVGLSET QNGGMSQEA VGNIKVTKSPQK STVLNTEAAMQSSNESKGGK MKKKRKMVNDAEPDTKKAKT ENKKGSEESAETTKETENNVE KPDNDESEVPSLPGLGTGAF EDTSFASLNLVNENTLKAIKE MGFTNMTEIQHKSIRPLEGRD LLAAAKTGSGKTLAFLIPAVELI VVKLRFMPRNGTGVILSPVRE LAMQTFGVKELMTHHVHTYG LIMGGSNRSAAQKLGNGINIIV ATPGRLLDHMQNTPGFMYKNL QCLVIDEADRLDVGFEELKQI IKLLPTRRQTMFSATQTRKVE DLARISLKKELPYVGVDDDKA NATVDGLEQGYVVCPEKRFL LLFTFLKKNRKKKLMVFFSSCM SVKYHYELLNYIDL/PVLAIHGK QKQNKRTTTFQFCNADSG/TL LCTDVAARGLDIPEVDWIVQY DPPDDPKETVHRVG*EQPEGLN GEEGHALASFLRPKDLGFFFR LL*KHSGFPLSGIWTFSW/SLK ISDIQFSAWRNWIGKVITFLHKS AQEAYKSYITEPMDSFPL*NRS FNIVNNLNLASGLLCQFGFK/VP PFVDLNVNSNEGKQKRGGGG GFGLPKRTQEKLEKS/KIF*TH* ARKSSGQAGQFSH

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 25 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/00, 15/12

US CL : 536/23.1, 23.5; 435/6, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.5; 435/6, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NONEElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)
NONE**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P ---	Database Genbank, Accession No. AL135937, 15 March 2001 (15.03.2001), particularly nucleotides 29925 through 30325.	1-8 ----- 9, 19
X ---	Database Genbank, Accession No. AA004350, HILLIER et al., Generation and analysis of 280,000 Human Expressed Sequence Tags. Genome Res. 07 May 1997 (07.05.1997), Vol. 6, No. 9, pages 807-828.	1-8 ----- 9, 19

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier applications or patent published on or after the international filing date
- *L* documents which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents; such combination being obvious to a person skilled in the art
- *Z* document member of the same patent family

Date of the actual completion of the international search

23 October 2001 (23.10.2001)

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

Box PCT

Washington, D.C. 20531

Facsimile No. (703)305-3230

Date of mailing of the international search report

02 JAN 2002

Authorized officer

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest

☐
☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I-III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct inventions.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.